

**LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT
& METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED
WITH BRONCHOCONSTRICTION, LUNG INFLAMMATION,
ALLERGY(IES) & SURFACTANT DEPLETION**

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BACKGROUND OF THE INVENTION

Field of the Invention

This patent relates to a composition comprising oligonucleotides (oligos) that are anti-sense to adenosine receptors, and contain low amounts of or no adenosine (A). These agents are suitable for the treatment, among others, of pulmonary diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. Examples of these diseases are allergies, asthma, impeded respiration, allergic rhinitis, pain, cystic fibrosis, and cancers such as leukemias, e.g. colon cancer, and the like. The present agent may be administered prophylactically or therapeutically in conjunction with other therapies, or may be utilized as a substitute for therapies that have significant, negative side effects.

Background of the Invention

Respiratory ailments, associated with a variety of diseases and conditions, are extremely common in the general population, and more so in certain ethnic groups, such as African Americans. In some cases they are accompanied by inflammation, which aggravates the condition of the lungs. Asthma, for example, is one of the most common diseases in industrialized countries. In the United States it accounts for about 1% of all health care costs. An alarming increase in both the prevalence and mortality of asthma over the past decade has been reported, and asthma is predicted to be the preeminent occupational lung disease in the next decade. While the increasing mortality of asthma in industrialized countries could be attributable to the depletion reliance upon beta agonists in the treatment of this disease, the underlying causes of asthma remain poorly understood.

Adenosine may constitute an important mediator in the lung for various diseases, including bronchial asthma. Its potential role was suggested by the finding that asthmatics respond favorably to aerosolized adenosine with marked bronchoconstriction whereas normal individuals do not. An asthmatic rabbit animal model, the dust mite allergic rabbit model for human asthma, responded in a similar fashion to aerosolized adenosine with marked bronchoconstriction whereas non-asthmatic rabbits showed no response. More recent work with this animal model suggested that adenosine-induced bronchoconstriction and bronchial hyperresponsiveness in asthma may be mediated primarily through the stimulation of adenosine receptors. Adenosine has also been shown to cause adverse effects, including death, when administered therapeutically for other diseases and conditions in subjects with previously undiagnosed hyper reactive airways.

A handful of medicaments have been available for the treatment of respiratory diseases and conditions, although in general they all have limitations. Theophylline, an important drug in the treatment of asthma, is a known adenosine receptor antagonist which was reported to eliminate adenosine-mediated bronchoconstriction in asthmatic rabbits. A selective adenosine A₁ receptor antagonist, 8-cyclopentyl-1, 3-dipropylxanthine (DPCPX) was also reported to inhibit adenosine-mediated bronchoconstriction and bronchial hyperresponsiveness in allergic rabbits. The therapeutic and preventative applications of currently available adenosine A₁ receptor-specific antagonists are, nevertheless, limited by their toxicity. Theophylline, for example, has been widely used in the treatment of asthma, but is associated with frequent, significant toxicity resulting from its narrow therapeutic dose range. DPCPX is far too toxic to be useful clinically. The fact that, despite decades of extensive research, no specific adenosine receptor antagonist is available for clinical use attests to the general toxicity of these agents. Anti-sense oligonucleotides have received considerable theoretical consideration as potential useful pharmacological agents in human disease. Their practical application in actual models of human disease, however, has been somewhat elusive. One important impediment to their effective application has been a difficulty in finding

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an appropriate route of administration to deliver them to their site of action. Many in vivo experiments were conducted by administering anti-sense oligonucleotides directly to specific regions of the brain. These applications, however, necessarily have limited clinical utility due to their invasive nature. Although anti-sense oligonucleotides have received considerable theoretical consideration for their potential use as pharmacological agents in human disease, finding practical and effective applications for these agents in actual models of human disease, however, have been few and far between, particularly because they had to be administered in large doses. Another important consideration in the pharmacologic application of these molecules is their route of administration. Many in vivo applications have involved the direct administration of anti-sense oligonucleotides to limited regions of the brain. Such applications, however, have limited clinical utility due to their invasive nature. The systemic administration of anti-sense oligonucleotides as pharmacological agents has been found to have also significant problems, not the least of which being an inherent difficulty in targeting disease-involved tissues. That is, the necessary dilution of the anti-sense oligonucleotide in the circulatory system makes extremely difficult to attain a therapeutic dose at the target tissue by intravenous or oral administration. The bioavailability of orally administered anti-sense oligonucleotides is very low, of the order of less than about 5%. Anti-sense oligonucleotides have been used in therapy by many, including the present inventor, who in his previous work successfully treated various diseases and conditions by direct administration of these agents to the lung. In many instances, other workers have had to face the difficulties associated with the delivery of DNA molecules to a desired target. Thus, the route of administration may be of extreme importance for treating generalized diseases and conditions as well as those which are localized. In contrast, up to the present time, the delivery of anti-sense agents to the lung has been relatively undeveloped. As described by the present inventor in more detail below, the lung is an excellent target for the direct administration of anti-sense oligonucleotides and provides a non-invasive and a tissue-specific route.

Clearly, there exist presently no effective therapies for treating these ailments, or at least no therapies which are effective and devoid of significant detrimental side effects. Accordingly, there is still a need for an agent for the treatment of adenosine mediated ailments afflicting the pulmonary and respiratory ailments affecting the lung airways, including respiratory problems, bronchoconstriction, inflammation, allergy(ies), depletion or hyposecretion of surfactant, etc., which is highly effective and sufficiently selective to avoid detrimental side effects produced by other therapies. In addition, there is a definite need for making available a delivery method that will require low amounts of therapeutic agents and will be effective for the rapid and targeted access of tissue genes of mRNAs and the reversal of untoward effects afflicting a subject.

SUMMARY OF THE INVENTION

The present invention generally relates to a pharmaceutical or veterinary composition, comprising an anti-sense oligonucleotide(s) (oligo(s)) which is (are) effective for alleviating bronchoconstriction and/or lung inflammation, allergy(ies), and/or surfactant depletion and/or hyposecretion, when administered to a mammal, the oligo containing about 0 to about 15% adenosine (A) and being anti-sense to a target selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; and a pharmaceutically or veterinarily acceptable carrier or diluent. The targets are typically molecules associated with airway disease, cancer, etc., such as transcription factors, stimulating and activating peptide factors, cytokines, cytokine receptors, chemokines, chemokine receptors, adenosine receptors, bradykinin receptors, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, binding proteins, and malignancy associated proteins, among others. Examples are oligo(s) targeted to adenosine receptor(s) and it(they) are typically

present in the composition in an amount effective to reduce adenosine mediated effect(s), such as airway obstruction, inflammation, allergy(ies), and surfactant depletion, among others. The adenosine receptor is preferably selected from the group consisting of the adenosine A₁, A_{2b}, and A₃ receptors, and in some instances even adenosine A_{2a} receptors. The oligo of the invention may be applied to the preparation of a medicament for (a) reducing adenosine-mediated bronchoconstriction, impeded respiration, inflammation, allergy(ies), depletion production of surfactant, and other detrimental pulmonary effects in a subject in need of treatment, and/or for (b) treating specific diseases and conditions such as asthma, cystic fibrosis, allergic rhinitis, COPD, etc. For the first time this invention provides the targeted administration of one or more oligonucleotides directly into the respiratory system. The oligos may be directed to any target and are intended for fast delivery through the mucosal tissue of the lungs for hybridization to a desired target polynucleotide, e. g. mRNA, to prevent gene transcription and translation, such that protein expression will be reduced, hampered, or completely stopped. Thus, this invention also provides a more general method for administering oligonucleotides that are anti-sense to targeted genes and mRNAs associated with any type of diseases, by direct administration into the respiratory system, e. g. by inhalation, by introduction of a solution or aerosol into the respiratory airways, and/or directly into the lung.

The present oligos, moreover, are suitable for reducing effects mediated by a variety of target proteins and genes, for example adenosine-mediated effects, including pulmonary, respiratory, and other associated effects, e. g. bronchoconstriction, inflammation, immune mediated reactions, allergy(ies) and other airway problems, which may be caused by different conditions, including cancer. Examples of diseases and conditions, which may be treated preventatively, prophylactically and therapeutically with the agent of this invention, are pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), bronchitis, and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The present agents are also suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. The present agent is effectively administered prophylactically and therapeutically in conjunction with other therapies, or by itself for conditions without known therapies or as a substitute for therapies that have significant negative side effects. The oligo(s) may be administered by any means known to a subject, e. g. to the lungs of the subject, more generally through any and all systemic and topical routes. This oligonucleotide(s) (oligo(s)) employed are anti-sense to to a target DNA or RNA, e. g. an adenosine receptor DNA or RNA, and preferably consist essentially of up to about 15% adenosine (A), and more preferably contain no adenosine. The oligos are provided in the form of specific compositions and formulations, with a carrier or diluent, and optionally with other therapeutic agents and additives which are used for administration by specific routes, e.g. into the respiratory system, topically, transdermally, parenterally, by implantation, and the like. The oligo is also provided as a capsule or cartridge, and in the form of a kit. The oligos of the invention may be produced by selection of specific targeted segments of the gene or mRNA encoding the adenosine receptor as described below. In one preferred embodiment, the selection is made to obtain oligos that consisting essentially of less than about 15% adenosine (A). This may be done by selecting the target as done above, which includes genes, genomic flanking regions, RNAs and polypeptide associated with an ailment afflicting the lung airways, obtaining the sequence of a mRNA(s) corresponding to the target gene(s) and/or their genomic flanking region(s) and/or the juxta-membrane regions thereof, and mRNA(s) encoding the target polypeptide(s), selecting at least one segment of the mRNA(s), and synthesizing one or more anti-sense oligonucleotide(s) to the selected mRNA segment(s), and substituting, if necessary, an alternative, e. g. a universal base(s) or other base(s) for one or more A to reduce the proportion of A present in the oligonucleotide to less than about 15%, and down to no adenosine. Similarly, alternative and/or universal bases may be substituted for adenosine, e. g. specific

adenosine A1, A2b and A3 receptor antagonists or A2a receptor agonists, theophylline, enprophylline, and many other adenosine receptor antagonists known in the art as well as agonists with significantly reduced agonist activity with respect to adenosine, e. g. less than 0.5%, less than 0.3%, and the like.

5 The invention will now be described in general in conceptual and experimental terms, with reference to specific examples. Other objects, advantages and features of the present invention will become apparent to those skilled in the art from the description that follows.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

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This invention arose from a desire by the inventor to improve on prior art treatments for pulmonary and other diseases, which technology is generally fraught with detrimental side effects and by the need of administering high doses of therapeutical agents. The present invention arises from the inventor's own discovery that adenosine receptor targeted anti-sense oligonucleotides (oligos) may be utilized therapeutically in the treatment of diseases or conditions which impair respiration, cause inflammation and/or allergy(ies), constrict bronchial tissue, obstruct the lung airways, depletion surfactant secretion, or otherwise impede normal breathing. In general, many diseases and conditions are associated with or cause inflammation, constrict bronchial tissue or the lung airways, depletion secretion of surfactant, augment allergy(ies), or otherwise impede normal breathing. This treatment is selective for specific targets associated with or mediating these symptoms, and the agents are administered in up to 1000-fold lower doses than those seen in the art. The inventor, in addition, wanted to provide a treatment which would improve the outcome and life style of patients undergoing other procedures or being administered other therapies, including antibody therapy, chemotherapy, radiation, phototherapy, and surgery e.g. cancer surgery, and that could be effectively administered preventatively, prophylactically or therapeutically. He reasoned that he could further improve on this discovery by selecting oligos of reduced adenosine content, or reducing the adenosine content of otherwise targeted anti-sense oligos corresponding to endogenous polynucleotide sequences. The present invention is premised on the discovery by the inventor that oligonucleotides are metabolized in vivo to their mononucleotides. Adenosine (A)-containing oligonucleotides break down and release adenosine which, in turn, activates adenosine receptors, thereby causing bronchoconstriction, inflammation, surfactant depletion, allergy(ies), and the like. He, thus, conceived of employing low adenosine-free adenosine oligos to avoid these side effects upon their administration. He succeeded in this endeavor and is providing in this patent novel and improved compositions, formulations and methods which afford greatly improved results when compared with previously known treatments for preventing and alleviating bronchoconstriction, allergy(ies), inflammation, breathing difficulties, surfactant depletion and blockage of airways, as well as for other conditions which affect the lung directly or indirectly. In different embodiments, one or more nucleic acids of the invention may be formulated alone, and/or with one or more surfactant components and/or with a carrier, and/or with other therapeutic agents and/or formulation agents known in the art. The compositions of this invention, thus, may be incorporated into a variety of formulations for systemic and topical administration. Moreover, the inventor also provides a broad method for delivery of anti-sense oligonucleotides (oligos) through the respiratory system, as a fast means of starting treatment to address acute attacks of asthma and other diseases and conditions that have a rapid onset. In addition, the present agents have long halflives and may be administered at very low doses. This makes them ideal for once a week type therapies. In the past, anti-sense oligonucleotides received considerable theoretical consideration as being potentially useful as pharmacologic agents for the treatment of human disease. Wagner, R., Nature 372: 333-335 (1994). However, it has been difficult to actually apply these molecules to alleviating and curing human diseases. One important consideration in the pharmacologic application of these molecules has been the failure of various routes of administration to deliver the compounds to its target while avoiding invading the circulation and, therefore, other untargeted tissues which, thus, produces a plethora of side effects. Most in vivo experiments utilizing anti-sense oligonucleotides involved a direct application of the oligo to limited regions of the brain. See, Wahlestedt, C., Trends in Pharmacol. Sci. 15: 42-46 (1994); Lai, J. et al., Neuroreport 5: 1049-1052 (1994); Standifer, K., et al., Neuron 12: 805-810

(1994); Akabayashi, A., et al., Brain Res. 21: 55-61 (1994). Others applied them into the spinal fluid. See, e.g. Tseng, L., et al., European J. Pharmacol. 258: R1-3 (1994); Raffa, R., et al., European J. Pharmacol. 258: R5-7 (1994); Gillardon, F., et al., European J. Neurosci. 6: 880-884 (1994). Such applications, clearly, have no practical clinical utility due to their invasive nature. Thus, the systemic administration of anti-sense oligonucleotides poses significant problems with respect to their pharmacologic application, not the least of which is the difficulty in selectively targeting disease-involved tissues. The systemic administration of anti-sense oligonucleotides also poses significant problems with respect to their pharmacologic application, not the least of which is the difficulty in selectively targeting disease-involved tissues.

The respiratory system, and in particular the lung, as the ultimate port of entry into the organism, however, is an excellent route of administration for anti-sense oligonucleotides. This is so not only for the treatment of lung disease, but also when utilizing the lung as a means for delivery, particularly because of its non-invasive and tissue-specific nature. Thus, local delivery of antisense oligonucleotides directly to the target tissue enables the therapeutic use of these compounds. Fomivirsen (ISIS 2302) is an example of a local drug delivery into the eye to treat cytomegalovirus (CMV) retinitis, for which a new drug application has been filed by ISIS. The administration of a drug through the lung offers the further advantage that inhalation is non-invasive whereas direct injection in to the vitreous of the eye is invasive. The composition and formulations of this invention are highly efficacious for preventing and treating diseases and conditions associated with bronchoconstriction, difficult breathing, impeded and obstructed lung airways, allergy(ies), inflammation and surfactant depletion, among others. Examples of diseases and conditions which are suitably treated by the present method are diseases and conditions, including Acute Respiratory Distress Syndrome (ARDS), asthma, adenosine administration e.g. in the treatment of SupraVentricular Tachycardia (SVT) and other arrhythmias, and in stress tests to hyper-sensitized individuals, ischemia, renal damage or failure induced by certain drugs, infantile respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), lung transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, including colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The invention will be described with respect to the adenosine receptors as targets, but is similarly applicable to any other target with respect to the pulmonary administration of anti-sense oligos. The examples provided below show a complete inhibition of such adenosine receptor associated symptoms in a rabbit model for human bronchoconstriction, allergy(ies) and inflammation as well as the elimination of the ability of the adenosine receptor agonist par excellence, adenosine, to cause bronchoconstriction in hyper-responsive monkeys, which are animal models for human hyper-responsiveness to adenosine receptor agonists. The pharmaceutical composition and formulations of the invention, therefore, are suitable for preventing and alleviating the symptoms associated with stimulation of adenosine receptors, such as the adenosine A₁ receptors. The compositions and formulations of this invention, thus, are also suitable for prevent the untoward side effects of adenosine-mediated hyperresponsiveness in certain individuals, which are generally seen in diseases affecting respiratory activity.

The method of the present invention may be used to treat airway diseases and conditions in a subject of any kind and for any reason, with the intention that the adenosine content of anti-sense compounds be minimized, reduced or eliminated so as to prevent its liberation upon anti-sense degradation. Examples of diseases and conditions, which may be treated preventatively, prophylactically and therapeutically with the compositions and formulations of this invention, are pulmonary vasoconstriction, inflammation, allergies, asthma, allergic rhinitis, impeded respiration, Acute Respiratory Distress Syndrome (ARDS), renal damage and failure associated with ischemia as well as the administration of certain drugs, side effects associated with adenosine administration e.g. in SupraVentricular Tachycardia (SVT) and in adenosine stress tests, infantile Respiratory Distress Syndrome (infantile RDS), ARDS, pain,

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cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), lung transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, metastatic cancer such as hepatic metastases, lung, breast and prostate metastases, among others. The present compositions and formulations are suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. The present compositions and formulations may also be administered effectively as a substitute for therapies that have significant negative side effects. The terms "anti-sense" oligonucleotides generally refers to small, synthetic oligonucleotides, resembling single-stranded DNA, which in this patent are applied to the inhibition of gene expression by inhibition of a target messenger RNA (mRNA). See, Milligan, J. F. et al., *J. Med. Chem.* 36(14), 1923-1937 (1993), the relevant portion of which is hereby incorporated in its entirety by reference. For consistency's sake, all RNAs and oligonucleotides are represented in this patent by a single strand in the 5' to 3' direction, when read from left to right, although their complementary sequence(s) is (are) also encompassed within the four corners of the invention. In addition, all nucleotide bases and amino acids are represented utilizing the recommendations of the IUPAC-IUB Biochemical Nomenclature Commission, or by the known 3-letter code (for amino acids). Nucleotide sequences are presented herein by single strand only, in the 5' to 3' direction, from left to right. In addition, nucleotide and amino acids are represented herein in the manner recommended by the IUPAC-IUB Biochemical Nomenclature Commission, or (for amino acids) by three letter code, in accordance with 37 CFR ' 1.822 and established usage. See, e.g., PatentIn User Manual, 99-102 (Nov. 1990) (U.S. Patent and Trademark Office, Office of the Assistant Commissioner for Patents, Washington, D.C. 20231); U.S. Patent No. 4,871,670 to Hudson et al. at col. 3, lines 20-43. The present method utilizes anti-sense agents to inhibit or down-regulate gene expression of target genes, including those listed in Tables 1 and 2 below. This is generally attained by hybridization of the anti-sense oligonucleotides to coding (sense) sequences of a targeted messenger RNA (mRNA), as is known in the art. The exogenously administered agents of the invention decrease the levels of mRNA and protein encoded by the target gene and/or cause changes in the growth characteristics or shapes of the thus treated cells. See, Milligan et al. (1993); Helene, C. and Toulme, J. *Biochim. Biophys. Acta* 1049, 99-125 (1990); Cohen, J. S. D., Ed., *Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression*; CRC Press: Boca Raton, FL (1987), the relevant portion of which is hereby incorporated in its entirety by reference. As used herein, "anti-sense oligonucleotide or anti-sense oligo" is generally a short sequence of synthetic nucleotide that (1) hybridizes to any segment of a mRNA encoding a targeted protein under appropriate hybridization conditions, and which (2) upon hybridization causes a decrease in gene expression of the targeted protein. The terms "desAdenosine" (desA) and "des-thymidine" (desT) refer to oligonucleotides substantially lacking either adenosine (desA) or thymidine (desT). In some instances, the des A or des T sequences are naturally occurring, and in others they may result from substitution of an undesirable nucleotide (A) by another lacking its undesirable activity, such as acting as an agonist or having a triggering effect at the adenosine A receptor(s). In the present context, the substitution is generally accomplished by substitution of A with a "universal or alternative base", presently known in the art or to be ascertained at a later time. As used herein, the terms "prevent", "preventing", "treat" or "treating" refer to a preventative, prophylactic, maintenance, or therapeutic treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms associated with adenosine receptor stimulation. The term "down-regulate" refers to inducing a decrease in production, secretion or availability and, thus, a decrease in concentration, of intracellular target product, be it a receptor e. g. adenosine A₁, A_{2b}, A₃, bradykinin 2B, GATA-3, or other receptors, or an increase in concentration of the adenosine A_{2a} receptor. The present technology relies on the design of anti-sense oligos targeted to mRNAs associated with ailments involving lung airway pathology(ies), and on their modification to reduce the occurrence of undesirable side effects caused by their release of adenosine upon breakdown, while preserving their activity and efficacy for their intended purpose. In this manner, the inventor targets a specific gene to

design one or more anti-sense oligonucleotide(s) (oligos) that selectively bind(s) to the corresponding mRNA, and then reduces, if necessary, their content of adenosine via substitution with an alternative or a universal base, or an adenosine analog incapable of significantly, or having substantially reduced ability for, activating or antagonizing adenosine A₁, A_{2b} or A₃ receptors or which may act as an agonist at the adenosine A_{2a} receptor. Any number of adenosines present may be substituted by an alternative and/or universal base, such as heteroaromatic bases, which binds to a thymidine base but has less than about 0.3 of the adenosine base agonist or antagonist activity at the adenosine A₁, A_{2a}, A_{2b} and A₃ receptors. Based on his prior experience in the field, the inventor reasoned that in addition to "downregulating" specific genes, he could increase the effect of the agent(s) administered by either selecting segments of RNA that are devoid, or have a low content, of thymidine (T) or, alternatively, substitute one or more adenosine(s) present in the designed oligonucleotide(s) with other nucleotide bases, so called universal bases, which bind to thymidine but lack the ability to activate adenosine receptors and otherwise exercise the constricting effect of adenosine in the lungs, etc. Given that adenosine (A) is a nucleotide base complementary to thymidine (T), when a T appears in the RNA, the anti-sense oligo will have an A at the same position.

In one aspect of this invention, the anti-sense oligonucleotide has a sequence which specifically binds to a portion or segment of a mRNA molecule which encodes a protein associated with impeded breathing, allergy(ies), lung inflammation, depletion of lung surfactant or lowering of lung surfactant, airway obstruction, bronchitis, and the like. One effect of this binding is to reduce or even prevent the translation of the corresponding mRNA and, thereby, reduce the available amount of target protein in the subject's lung. In one preferred embodiment of this invention, the phosphodiester residues of the anti-sense oligonucleotide are modified or substituted. Chemical analogs of oligonucleotides with modified or substituted phosphodiester residues, e.g., to the methylphosphonate, the phosphotriester, the phosphorothioate, the phosphorodithioate, or the phosphoramidate, α -methoxy ethyl and similar modifications, which increase the in vivo stability of the oligonucleotide are particularly preferred. The naturally occurring phosphodiester linkages of oligonucleotides are susceptible to some degree of degradation by cellular nucleases. Many of the residues proposed herein, on the contrary, are highly resistant to nuclease degradation. See, Milligan et al.; Cohen, J. S. D., supra. In another preferred embodiment of the invention, the oligonucleotides may be protected from degradation by adding a "3'-end cap" by which nuclease-resistant linkages are substituted for phosphodiester linkages at the 3' end of the oligonucleotide. See, Tidd, D. M. and Warenius, H.M., *Be. J. Cancer* 60: 343-350 (1989); Shaw, J.P. et al., *Nucleic Acids Res.* 19: 747-750 (1991), the relevant section of which are incorporated in their entireties herein by reference. Phosphoramidates, phosphorothioates, and methylphosphonate linkages all function adequately in this manner for the purposes of this invention, as do α' modifications, such as α' methoxy ethyl, and the like. The more extensive the modification of the phosphodiester backbone the more stable the resulting agent, and in many instances the higher their RNA affinity and cellular permeation. See, Milligan, et al., supra. In addition, a plurality of substitutions to the carbohydrate ring are also known to improve stability of nucleic acids. Thus, the number of residues which may be modified or substituted will vary depending on the need, target, and route of administration, and may be from 1 to all the residues, to any number in between. Many different methods for replacing the entire phosphodiester backbone with novel linkages are known. See, Millikan et al, supra. Preferred backbone analogue residues include phosphoramidate, phosphorothioate, methylphosphonate, phosphotriester, phosphotriester, thioformacetal, phosphorodithioate, phosphoramidate, formacetal, triformacetal, thioether, carbamate, boranophosphate, 3'-thioformacetal, 5'-thioether, carbonate, C₅-substituted nucleotides, 5'-N-carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, 2'-O methyl, sulfoxide, sulfide, hydroxylamine, methylene(methylimino) (MMI), methoxymethyl (MOM), and methoxyethyl(MOE), and methyleneoxy(methylimino) (MOMI) residues, and combinations thereof. Phosphorothioate and methylphosphonate-modified oligonucleotides are particularly preferred due to their availability through automated oligonucleotide synthesis. See, Millikan et al, supra. Where appropriate, the agent of this

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invention may be administered in the form of their pharmaceutically acceptable salts, or as a mixture of the anti-sense oligonucleotide and its salt. In another embodiment of this invention, a mixture of different anti-sense oligonucleotides or their pharmaceutically acceptable salts is administered. A single agent of this invention has the capacity to attenuate the expression of a target mRNA and/or various agents to enhance or attenuate the activity of a pathway. By means of example, the present method may be practiced by identifying all possible deoxyribonucleotide segments which are low in thymidine (T) or deoxynucleotide segments low in adenosine (A) of about 7 or more mononucleotides, preferably up to about 60 mononucleotides, more preferably about 10 to about 36 mononucleotides, and still more preferably about 12 to about 21 mononucleotides, in a target mRNA or a gene, respectively. This may be attained by searching for mononucleotide segments within a target sequence which are low in, or lack thymidine (RNA), a nucleotide which is complementary to adenosine, or that are low in adenosine (gene), that are 7 or more nucleotides long. In most cases, this search typically results in about 10 to 30 such sequences, i.e. naturally lacking or having less than about 40% adenosine, anti-sense oligonucleotides of varying lengths for a typical target mRNA of average length, i.e., about 1800 nucleotides long. Those with high content of T or A, respectively, may be fixed by substitution of a universal base for one or more As. The agent(s) of this invention may be of any suitable length, including but not limited to, about 7 to about 60 nucleotides long, preferably about 12 to about 45, more preferably up to about 30 nucleotides long, and still more preferably up to about 21, although they may be of other lengths as well, depending on the particular target and the mode of delivery. The agent(s) of the invention may be directed to any and all segments of a target RNA. One preferred group of agent(s) includes those directed to an mRNA region containing a junction between an intron and an exon. Where the agent is directed to an intron/exon junction, it may either entirely overlie the junction or it may be sufficiently close to the junction to inhibit the splicing-out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g. with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, within about 2 to 10, preferably about 3 to 5, nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon, and those near the 5' and 3' termini of the coding region. The flanking regions of the exons may also be targeted as well as the spliced segments in the precursor mRNAs. The mRNA sequences of the adenosine receptors and of many other targets are derived from the DNA base sequence of the gene expressing either receptors, e. g. the adenosine receptors, the enzymes, factors, or other targets associated with airway disease. For example, the sequence of the genomic human A₁ adenosine receptor is known and is disclosed in U.S. Patent No. 5,320,963 to Stiles, G., et al. The A₃ adenosine receptor has been cloned, sequenced and expressed in rat (see, Zhou, F., et al., P.N.A.S. (USA) 89: 7432 (1992)) and human (see, Jacobson, M. A., et al., U.K. Patent Application No. 9304582.1 (1993)). The sequence of the adenosine A_{2b} receptor gene is also known. See, Salvatore, C. A., Luneau, C. J., Johnson, R. G. and Jacobson, M., Genomics (1995), the relevant portion of which is hereby incorporated in its entirety by reference. The sequences of many of the remaining exemplary target genes are also known. See, GenBank, NIH. The sequences of those genes whose sequences are not yet available may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, an anti-sense oligonucleotides may be produced according to this invention as described above to reduce the production of the targeted protein in accordance with standard techniques. The sequences for the adenosine A_{2a} bradykinin, and other genes as well as methods for preparation of oligonucleotides are also known as those of many other target genes and mRNAs for which this invention is suitable. Thus, anti-sense oligonucleotides that downregulate the production of target sequences associated with airway disease, including the adenosine A₁, A_{2a}, A_{2b}, A₃, bradykinin, GATA-3, COX-2, and many other receptors, may be produced in accordance with standard techniques. Examples of diseases and conditions which are suitably treated by the present method are diseases and conditions, including Acute Respiratory Distress Syndrome (ARDS), asthma, adenosine administration e.g. in the treatment of SupraVentricular Tachycardia (SVT) and other arrhythmias, and in stress tests to hyper-sensitized individuals, ischemia, renal damage or failure induced by certain drugs, infantile respiratory distress

syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, including colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer.

The adenosine receptors discussed above are mere examples of the high power of the inventor's technology. In fact, a large number of genes may be targeted in a similar manner by the present agent(s), to reduce or down-regulate protein expression. By means of example, if the target disease or condition is one associated with impeded or reduced breathing, bronchoconstriction, chronic bronchitis, pulmonary bronchoconstriction and/or hypertension, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, allergy, asthma, cystic fibrosis, respiratory distress syndrome, cancers, which either directly or by metastasis afflict the lung, the present method may be applied to a list of potential target mRNAs, which includes the targets listed in Table 1 and Table 2 below, among others. The anti-sense agent(s) of the invention have a low A content to prevent its liberation upon in vivo degradation of the agent(s). For example, if the system is the pulmonary or respiratory system, a large number of genes is involved in different functions, including those listed in Table 1 below.

Table 1: Pulmonary Disease or Condition Pulmonary and Inflammation Targets

Nf6B Transcription Factor	Interleukin-8 Receptor (IL-8 R)
20 Interleukin-5 Receptor (IL-5R)	Interleukin-4 Receptor (IL-4R)
Interleukin-3 Receptor (IL-3R)	Interleukin-1 β (IL-1 β)
Interleukin-1 β Receptor (IL-1 β R)	Eotaxin
Tryptase	Major Basic Protein
β 2-adrenergic Receptor Kinase	Endothelin Receptor A
25 Endothelin Receptor B	Preproendothelin
Bradykinin B2 Receptor (B2BR)	IgE (High Affinity Receptor)
Interleukin-1 (IL-1)	Interleukin 1 Receptor (IL-1 R)
Interleukin-9 (IL-9)	Interleukin-9 Receptor (IL-9 R)
Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11 R)
30 Inducible Nitric Oxide Synthase	Cyclooxygenase (COX)
Intracellular Adhesion Molecule 1 (ICAM-1)	Vascular Cellular Adhesion Molecule (VCAM)
Substance P	Endothelial Leukocyte Adhesion Molecule Endothelin ETA
Rantes	(ELAM-1)
Receptor	GM-CSF, Endothelin-1
35 Cyclooxygenase-2 (COX-2)	Neutrophil Chemotactic Factor
Monocyte Activating Factor	Defensin 1,2,3
Neutrophil Elastase	Platelet Activating Factor
Muscarinic Acetylcholine Receptors	5-lipoxygenase
Tumor Necrosis Factor α	Substance P
40 Phosphodiesterase IV	Histamine Receptor
Substance P Receptor	CCR-1 CC Chemokine Receptor
Chymase	Interleukin-4 (IL-4)
Interleukin-2 (IL-2)	Interleukin-5 (IL-5)
Interleukin-12 (IL-12)	Interleukin-7 (IL-7)
45 Interleukin-6 (IL-6)	Interleukin-12 Receptor (IL-12R)
Interleukin-8 (IL-8)	Interleukin-1 (IL-1)
Interleukin-7 Receptor (IL-7R)	Interleukin-14
Interleukin-14 Receptor (IL-14R)	CCR-3 CC Chemokine Receptor
CCR-2 CC Chemokine Receptor	CCR-5 CC Chemokine Receptor
50 CCR-4 CC Chemokine Receptor	GATA-3 Transcription Factor
Prostanoid Receptors	MAP Kinase
Neutrophil Adherence Receptor	Interleukin-15 Receptor (IL-15R)
Interleukin-15 (IL-15)	

	Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11R)
	NFAT Transcription Factors	STAT 4
	MIP-1 α	MCP-2
	MCP-3	MCP-4
5	Cyclophilin (A, B, etc.)	Phospholipase A2
	Basic Fibroblast Growth Factor	Metalloproteinase
	CSBP/p38 MAP Kinase	Tryptase Receptor
	PDG2	Interleukin-3 (IL-3)
	Interleukin-10 (IL-10)	Cyclosporin A - Binding Protein
10	FK506-Binding Protein	α 4 β 1 Selectin
	Fibronectin	α 4 β 7 Selectin

Table 1: Pulmonary Disease or Condition Pulmonary and Inflammation Targets

	cMad CAM-1	LFA-1 (CD11a/CD18)
	PECAM-1	LFA-1 Selectin
15	C3bi	PSGL-1
	E-Selectin	P-Selectin
	CD-34	L-Selectin
	p150,95	Mac-1 (CD11b/CD18)
	Fucosyl transferase	VLA-4
20	STAT-1	STAT-2
	CD-18/CD11a	CD11b/CD18
	ICAM2 and ICAM3	C5a
	CCR3 (Eotaxin Receptor)	CCR1, CCR2, CCR4, CCR5
	LTB-4	AP-1 Transcription Factor
25	Protein kinase C	Cysteinyl Leukotriene Receptor
	Tachykinin Receptors (tach R)	I6B Kinase 1 & 2
	Interleukin-2 Receptor (IL-2R)	(e.g., Substance P, NK-1 & NK-3 Receptors)
	STAT 6	c-mas
	NF-Interleukin-6 (NF-IL-6)	Interleukin-10 Receptor (IL-10R)
30	Interleukin-3 (IL-3)	Interleukin-2 Receptor (IL-2R)
	Interleukin-13 (IL-13)	Interleukin-12 Receptor (IL-12R)
	Interleukin-14 (IL-14)	Interleukin-6 Receptor (IL-6R)
	Interleukin-16 (IL-16)	Interleukin-13 Receptor (IL-13R)
	Medullasin	Interleukin-16 Receptor (IL-16R)
35	Adenosine A ₁ Receptor (A ₁ R)	Tryptase-I
	Adenosine A _{2b} Receptor (A _{2b} R)	Adenosine A ₃ Receptor (A ₃ R)
	β Tryptase	STAT-3
	Adenosine A _{2a} Receptor (A _{2a} R)	IgE Receptor β Subunit (IgE R β)
	Fc-epsilon receptor CD23 antigen	IgE Receptor α Subunit (IgE R α)
40	IgE Receptor Fc Epsilon Receptor (IgERFc ξ R)	Substance P Receptor
	Histidine decarboxylase	Tryptase-1
	Prostaglandin D Synthase	Eosinophil Cationic Protein
	Eosinophil Derived Neurotoxin	Eosinophil Peroxidase
	Endothelial Nitric Oxide Synthase	Endothelial Monocyte Activating Factor
45	Neutrophil Oxidase Factor	Cathepsin G
	Macrophage Inflammatory Protein-1-Alpha/Rantes Receptor	Interleukin-8 Receptor α Subunit (IL-8 R α)
		Endothelin Receptor ET-B

These genes, and others, are involved in the normal functioning of respiration as well as in diseases associated with respiratory pathologies, including cystic fibrosis, asthma, pulmonary hypertension and vasoconstriction, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, chronic bronchitis, respiratory distress syndrome (ARDS), allergic rhinitis, lung

among others, have been shown to be effective in down-regulating the expression of their genes. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by "down regulation" of the adenosine A₁, A_{2a}, A_{2b}, and/or A₃ receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents may be utilized by the present method alone or in conjunction with anti-sense oligos targeted to other genes to validate pathway and/or networks in which they are involved. For better results, the oligos are preferably administered directly into the respiratory system, e.g., by inhalation or other means, of the experimental animal, so that they may reach the lungs without widespread systemic dissemination. This permits the use of low agent doses as compared with those administered systemically or by other generalized routes and, consequently, reduces the number and degree of undesirable side effects resulting from the agent=s widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity. Anti-sense oligonucleotides to the A₁, A_{2b}, A₃, bradykinin B2, GATA-3, CAM (vascular cell adhesion molecule), eosinophil receptors, and COX-2 receptors, among others, have been shown to be effective in the down-regulation of the respective receptor proteins in the cell. One novel feature of this treatment, as compared to traditional treatments for adenosine-mediated bronchoconstriction, is that administration is direct to the lungs, or in situ to other tissues, organs or systems of the body. Additionally, a receptor protein itself is reduced in amount, rather than merely interacting with a drug, and toxicity is reduced. Other proteins that may be targeted with anti-sense agents for the treatment of lung conditions include, but are not limited to: CCR3 (chemokine) receptors, human A_{2a} adenosine receptor, human A_{2b} adenosine receptor, human IgE receptor β , human Fc-epsilon receptor CD23 antigen, human histidine decarboxylase, human beta tryptase, human tryptase-I, human prostaglandin D synthase, human cyclooxygenase-2, human eosinophil cationic protein, human eosinophil derived neurotoxin, human eosinophil peroxidase, human intercellular adhesion molecule-1 (ICAM-1), human vascular cell adhesion molecule-1 (VCAM-1), human endothelial leukocyte adhesion molecule-1 (ELAM-1), human P selectin, human endothelial monocyte activating factor, human IL-3, human IL-4, human IL-5, human IL-6, human IL-8, human monocyte-derived neutrophil chemotactic factor, human neutrophil elastase, human neutrophil oxidase factor, human cathepsin G, human defensin 1, human defensin 3, human macrophage inflammatory protein-1-alpha, human muscarinic acetylcholine receptor HM3, human fibronectin, human GM-CSF, human tumor necrosis factor α , human leukotriene C4 synthase, human major basic protein, and human endothelin 1. Although not intended to be exclusive, a more extensive list of genes is provided below. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by "down regulation" of the adenosine A₁, A_{2a}, A_{2b}, and/or A₃ receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents are preferably administered directly into the respiratory system, e.g., by inhalation or other means, so that they may reach the lungs without widespread systemic dissemination. This permits the use of substantially lower doses of the agent of the invention as compared with those administered by the prior art, systemically or by other generalized routes and, consequently, reduce undesirable side effects resulting from the agent=s widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity. In these latter targets, and in target genes in general, it is particularly imperative to eliminate or reduce the adenosine content of the corresponding anti-sense oligonucleotide to prevent their breakdown products from liberating adenosine.

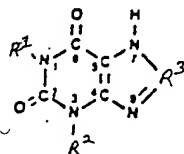
As used herein, the term "treat" or "treating" asthma refers to a treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms of the lung disease. The term "downregulate" refers to inducing a decrease in production, secretion or availability (and thus a

decrease in concentration) of the targeted intracellular protein. The present invention is concerned primarily with the treatment of human subjects. However, the agents and methods disclosed here may also be employed for veterinary purposes, such as is the case in the treatment of other mammals, such as cattle, horses, wild animals, zoo animals, and domestic animals, e. g. dogs and cats. Targeted proteins are preferably mammalian and more preferably of the same species as the subject being treated. In general, "anti-sense" refers to the use of small, synthetic oligonucleotides, resembling single-stranded DNA, to inhibit gene expression by inhibiting the function of the target messenger RNA (mRNA). Milligan, J. F. et al., *J. Med. Chem.* 36(14), 1923-1937 (1993). In the present invention, inhibition of gene expression of the A₁ or A₃ adenosine receptor is desired. Gene expression is inhibited through hybridization to coding (sense) sequences in a specific messenger RNA (mRNA) target by hydrogen bonding according to Watson-Crick base pairing rules. The mechanism of anti-sense inhibition is that the exogenously applied oligonucleotides decrease the mRNA and protein levels of the target gene or cause changes in the growth characteristics or shapes of the cells. Id. See, also Helene, C. and Toulme, J., *Biochim. Biophys. Acta* 1049, 99-125 (1990); Cohen, J. S. D., Ed., *Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression*; CRC Press: Boca Raton, FL (1987). As used herein, "anti-sense oligonucleotide" is defined as a short sequence of synthetic nucleotide that (1) hybridizes to any coding sequence in an mRNA which codes for the targeted protein, according to hybridization conditions described below, and (2) upon hybridization causes a decrease in gene expression of the A₁ or A₃ adenosine receptor. The receptors discussed above are mere examples of the high power of the present technology. In fact, a large number of genes may be targeted in a similar manner by practicing the present methods, to significantly down-regulate or obliterate protein expression and observe any changes wrought to one or more functions within a system, e.g. the respiratory system and other lung disease associated targets. By means of example, in the respiratory system, the targets may be associated with difficulties of breathing, bronchoconstriction, inflammation, allergic rhinitis, chronic bronchitis, surfactant depletion, and others associated with diseases and conditions such as chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, inhalation burns, Acute Respiratory Distress Syndrome (ARDS), cystic fibrosis, pulmonary fibrosis, radiation pneumonitis, tonsillitis, emphysema, dental pain, oral inflammation, joint pain, esophagitis, cancers afflicting the respiratory system either directly such as lung cancer, esophageal cancer, and the like, or indirectly by means of metastases, among others. These functions are of great interest because of their association with respiratory dysfunction, as is the case in asthma, allergies, allergic rhinitis, pulmonary bronchoconstriction and hypertension, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, allergy, asthma, cystic fibrosis (CF), Acute Respiratory Distress Syndrome (ARDS) as well as infantile and pregnancy-related RDS, cancer, etc., which either directly or by metastasis afflict the lung, the present anti-sense oligonucleotides may be directed to a list of target mRNAs, which includes the targets listed in Table 1 above, among others.

The oligos of this invention may be obtained by first selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C and/or having a specific type and/or extent of activity, and then obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a thymidine (T) nucleic acid content of up to and including about 15%, preferably, about 12%, about 10%, about 7%, about 5%, about 3%, about 1%, and more preferably no thymidine. The latter step may be conducted by obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an adenosine base content of up to and including about 15%, preferably about 12%, about 10%, about 7%, about 5%, about 3%, about 1%, and more preferably no adenosine. When the selected fragment comprises at least one thymidine base, an adenosine base may be substituted in the corresponding anti-sense nucleotide fragment with a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have less than about 10%, preferably less than about 1%, and more preferably less than about 0.3% of the adenosine base agonist activity at the adenosine A₁, A_{2a}, A_{2b} and A₃ receptors, and heteroaromatic bases which have no activity at the adenosine

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A_{2a} receptor, when validating in the respiratory system. Other adenosine activities in other systems may be determined in other systems, as appropriate. The analogue heteroaromatic bases may be selected from all pyrimidines and purines, which may be substituted by O, halo, NH₂, SH, SO, SO₂, SO₃, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH₂, primary, secondary and tertiary amine, SH, SO, SO₂, SO₃, cycloalkyl, heterocycloalkyl and heteroaryl. The pyrimidines and purines may be substituted at all positions as is known in the art, but preferred are those which are substituted at positions 1, 2, 3, 4, 7 and/or 8. More preferred are pyrimidines and purines such as theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R¹ and R² are independently H, alkyl, alkenyl or alkynyl and R³ is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH₂-alkylamino-ketoxymethoxy-aryl, mono and dialkylaminoalkyl-N-alkylamino-SO₂aryl, among others. Similar modifications in the sugar are also embodiments of this invention. Reduced adenosine content of the anti-sense oligos corresponding to the thymidines (T) present in the target RNA serves to prevent the breakdown of the oligos into products that free adenosine into the system, e.g. the lung, brain, heart, kidney, etc., tissue environment and, thereby, to prevent any unwanted effects due to it. By means of example, the NF6B transcription factor may be selected as a target, and its mRNA or DNA searched for low thymidine (T) or desthymidine (desT) fragments. Only desT segments of the mRNA or DNA are selected which, in turn, will produce desA anti-sense as their complementary strand. When a number of RNA desT segments are found, the sequence of the anti-sense segments may be deduced. Typically, about 10 to 30 and even larger numbers of desA anti-sense sequences may be obtained. These anti-sense sequences may include some or all desA anti-sense oligonucleotide sequences corresponding to desT segments of the mRNA of the target, such as anyone of those shown in Table 1 above, in Table 2 below, and others associated with functions of the brain, cardiovascular and renal systems, and many others. When this occurs, the anti-sense oligonucleotides found are said to be 100% A-free. For each of the original desA anti-sense oligonucleotide sequences corresponding to the target gene, e.g. the NF6B transcription factor, typically about 10 to 30 sequences may be found within the target gene or RNA which have a low content of thymidine (RNA). In accordance with this invention, the selected fragment sequences may also contain a small number of thymidine (RNA) nucleotides within the secondary or tertiary or quaternary sequences. In some cases, a large adenosine content may suffice to render the anti-sense oligonucleotide less active or even inactive against the target. In accordance with this invention, these so called "non-fully desA" sequences may preferably have a content of adenosine of less than about 15%, about 12%, about 10%, about 7%, about 5%, and about 2% adenosine. Most preferred is no adenosine content (0%). In some instances, however, a higher content of adenosine is acceptable and the oligonucleotides still fail to show detrimental "adenosine activity". A particular important embodiment is that where the adenosine nucleotide is "fixed" or replaced by a "Universal or alternative" base that may base-pair with similar or equal affinity to two or more of the four nucleotide present in natural DNA: A, G, C, and T.

A universal or alternative base is defined in this patent as any compound, more commonly an

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adenosine analogue, which has substantial capacity to hybridize to thymidine, while at the same time having reduced, or substantially lacking, ability to bind adenosine receptors or other molecules through which adenosine may exert an undesirable side effect in the experimental animal or in a cell system. Alternatively, adenosine analogs which completely fail to activate, or have significantly reduce ability for activating, adenosine receptors, such as the adenosine A₁, A_{2b} and/or A₃ receptors, most preferably A₁ receptors, and those that may even act as agonists of the adenosine A_{2a} receptor, may be used. One example of a universal base is α -deoxyribofuranosol-(5-nitroindole), and an artisan will know how to select others. This "fixing" step generates further novel sequences, different from those anti-sense to the ones found in nature, that permits the anti-sense oligonucleotide to bind, preferably equally well, with the target RNA. Other examples of universal or alternative bases are 2-deoxyribosyl-(5-nitroindole). Other examples of universal bases are 3 - nitropyrrole - 2' - deoxynucleoside, 5 - nitro-indole, 2 - deoxyribosyl - (5 - nitroindole), 2-deoxyribofuranosyl - (5-nitroindole), 2' - deoxyinosine, 2' -deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4, 5 - c] oxazine - 7 - one and 2 - amino - 6 -methoxy aminopurine. In addition to the above, Universal bases which may be substituted for any other base although with somewhat reduced hybridization potential, include 3 - nitropyrrole 2' - deoxynucleoside 2 - deoxyribofuranosyl - (5 - nitroindole), 2' - deoxyinosine and 2' - deoxynebularine (Glen Research, Sterling, VA). More specific mismatch repairs may be made using "P" nucleotide, 6H, 8H - 3, 4 - dihydropyrimido [4,5 - c] [1, 2] oxazin - 7 - one, which base pairs with either guanine (G) or adenine (A) and "K" nucleotide, 2 - amino - 6 - methoxyaminopurine, which base pairs with either cytidine (C) or thymidine (T), among others. Others which are known in the art or will become available are also suitable. See, for example, Loakes, D. and Brown, D. M., Nucl. Acids Res. 22:4039-4043 (1994); Ohtsuka, E. et al., J. Biol. Chem.260(5):2605-2608 (1985); Lin, P.K.T. and Brown, D. M., Nucleic Acids Res. 20(19):5149-5152 (1992; Nichols, R. et al., Nature 369(6480): 492-493 (1994); Rahmon, M. S. and Humayun, N. Z., Mutation Research 377 (2): 263-8 (1997); Amosova, O., et al., Nucleic Acids Res. 25 (10): 1930-1934 (1997); Loakes D. & Brown, D. M., Nucleic Acids Res. 22 (20): 4039-4043 (1994), the entire sections relating to universal bases and their preparation and use in nucleic acid binding being incorporated herein by reference. When non-fully desT sequences are found in the naturally occurring target, they typically are selected so that about 1 to 3 universal base substitutions will suffice to obtain a 100% "desA" anti-sense oligonucleotide. Thus, the present method provides either anti-sense oligonucleotides to different targets which are low in, or devoid of, A content, as well as anti-sense oligonucleotides where one or more adenosine nucleotides, e. g. about 1 to 3, or more, may be "fixed" by replacement with a "Universal" or "replacement" base. Universal bases are known in the art and need not be listed herein. An artisan will know which bases may act as universal bases, and replace them for A. Table 2 below provides a selected number of targets to which the agents of the invention are effectively applied. Others, however, may also be targeted.

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Table 2: Cancer Targets	
Transforming Oncogenes	Therapy Targets
ras	thymidylate synthetase
src	thymidylate synthetase
myc	dihydrofolate reductase
bcl-2	thymidine kinase
	deoxycytidine kinase
	ribonucleotide reductase
Angiogenesis factors	Adhesion Molecules
Oncogenes	Folate Pathway Enzymes
DNA repair genes	(One Carbon Pool)
	Telomerase
	HMG CoA Reductase
	Farnesyl Transferase
	Glucose-6-Phosphate Transferase

A group of preferred targets for the treatment of cancer are genes associated with any of different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and BCL-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like. The present technology is particularly useful in the treatment of cancer ailments given that traditional cancer therapies are fraught with the unresolved problem of selectively killing cancer cells while preserving normal living cells from the devastating effects of treatments such as chemotherapy, radiotherapy, and the like. The present technology provides the ability of selectively attenuating or enhancing a desired pathway or target. This approach provides a significant advantage over standard treatments of cancer because it permits the selection of a pathway, including primary, secondary and possibly tertiary targets, which are not generally expressed simultaneously in normal cells. Thus, the present agent may be administered to a subject to cause a selective increase in toxicity within tumor cells that, for instance, express all three targets while normal cells that may express only one or two of the targets will be significantly less affected or even spared. A group of preferred targets for the treatment of cancers are genes associated with different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and BCL-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like.

In one embodiment, at least one of the mRNAs to which the oligo of the invention is targeted encodes a protein such as transcription factors, stimulating and activating factors, intracellular and extracellular receptors and peptide transmitters in general, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, and binding proteins, among others; or the mRNA is corresponding to an oncogene and other genes associated with various diseases or conditions. Examples of target proteins are eotaxin, major basic protein, preproendothelin, eosinophil cationic protein, P-selectin, STAT 4, MIP-1 α , MCP-2, MCP-3, MCP-4, STAT 6, c-mas, NF-IL-6, cyclophilins, PDG2, cyclosporin A-binding protein, FK5-binding protein, fibronectin, LFA-1 (CD11a/CD18), PECAM-1, C3bi, PSGL-1, CD-34, substance P, p150,95, Mac-1 (CD11b/CD18), VLA-4, CD-18/CD11a, CD11b/CD18, C5a, CCR1, CCR2, CCR4, CCR5, and LTB-4, among others. Others are, however, suitable, as well. In another embodiment, at least one of the mRNAs to which the oligo is targeted encodes intracellular and extracellular receptors and peptide transmitters such as sympathomimetic receptors, parasympathetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohipophyseal receptors, adenohipophyseal peptide transmitters, and histamine receptors (HisR), among others. However others are also contemplated. The encoded sympathomimetic receptors and parasympathomimetic receptors include acetylcholinesterase receptors (AcChaseR) acetylcholine receptors (AcChR), atropine receptors, muscarinic receptors, epinephrine receptors (EpiR), dopamine receptors (DOPAR), and norepinephrine receptors (NEpiR), among others. Further examples of encoded receptors are adenosine A₁ receptor, adenosine A₂B receptor, adenosine A₃ receptor, endothelin receptor A, endothelin receptor B, IgE high affinity receptor, muscarinic acetylcholine receptors, substance P receptor, histamine receptor, CCR-1 CC chemokine receptor, CCR-2 CC chemokine receptor, CCR-3 CC chemokine receptor (Eotaxin Receptor), interleukin-1 β receptor (IL-1 β R), interleukin-1 receptor (IL-1R), interleukin-1 β receptor (IL-

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- 1 β R), interleukin-3 receptor (IL-3R), CCR-4 CC chemokine receptor, cysteinyl leukotriene receptors, prostanoid receptors, GATA-3 transcription factor receptor, interleukin-1 receptor (IL-1R), interleukin-4 receptor (IL-4R), interleukin-5 receptor (IL-5R), interleukin-8 receptor (IL-8R), interleukin-9 receptor (IL-9R), interleukin-11 receptor (IL-11R), bradykinin B2 receptor, sympathomimetic receptors, 5 parasymphomimetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adenohipophyseal receptors, and histamine receptors (HisR). Others are also contemplated even though not listed herein. The encoded enzymes for development of the oligos of the invention include
- 10 synthetases, kinases, oxidases, phosphatases, reductases, polysaccharide, triglyceride, and protein hydrolases, esterases, elastases, and , polysaccharide, triglyceride, lipid, and protein synthases, among others. Examples of target enzymes are tryptase, inducible nitric oxide synthase, cyclooxygenase (Cox), MAP kinase, eosinophil peroxidase, β 2-adrenergic receptor kinase, leukotriene c-4 synthase, 5-lipoxygenase, phosphodiesterase IV, metalloproteinase, tryptase, CSBP/p38 MAP kinase, neutrophil
- 15 elastase, phospholipase A₂, cyclooxygenase 2 (Cox-2), fucosyl transferase, chymase, protein kinase C, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, and ribonucleotide reductase, among others. Any enzyme associated with a disease or condition, however, is suitable as a target for this invention. Suitable encoded factors for application of this invention are, among others, Nf6B transcription factor, granulocyte macrophage colony stimulating factor (GM-CSF), AP-1
- 20 transcription factor, GATA-3 transcription factor, monocyte activating factor, neutrophil chemotactic factor, granulocyte/macrophage colony-stimulating-factor (G-CSF), NFAT transcription factors, platelet activating factor, tumor necrosis factor α (TNF α), and basic fibroblast growth factor (BFGF). Additional factors are also within the invention even though not specifically mentioned. Suitable adhesion molecules for use with this invention include intracellular adhesion molecules 1 (ICAM-1), 2 (ICAM-2) and 3
- 25 (ICAM-3), vascular cellular adhesion molecule (VCAM), endothelial leukocyte adhesion molecule-1 (ELAM-1), neutrophil adherence receptor, mad CAM-1, and the like. Other known and unknown factors (at this time) may also be targeted herein. Among the cytokines, lymphokines and chemokines preferred are interleukin-1 (IL-1), interleukin-1 β (IL-1 β), interleukin-3 (IL-3), interleukin-4 (IL-4), interleukin-5 (IL-5), interleukin-8 (IL-8), interleukin-9 (IL-9), interleukin-11 (IL-11), CCR-5 CC chemokine, and Rantes.
- 30 Others, however, may also be targeted, as they are known to be involved in specific diseases or conditions to be treated, or for their generic activities, such as inflammation. Examples of defensins for the practice of this invention are defensin 1, defensin 2, and defensin 3, and of selectins are α 4 β 1 selectin, α 4 β 7 selectin, LFA-1 selectin, E-selectin, P-selectin, and L-selectin. Examples of oncogenes, although not an all inclusive list, are ras, src, myc, and bcBCL. Others, however, are also suitable for use with this invention.
- 35 The agents administered in accordance with this invention are preferably designed to be anti-sense to target genes and/or mRNAs related in origin to the species to which it is to be administered. When treating humans, the agents are preferably designed to be anti-sense to a human gene or RNA. The agents of the invention encompass oligonucleotides which are anti-sense to naturally occurring DNA and/or RNA sequences, fragments thereof of up to a length of one (1) base less than the targeted sequence, preferably at
- 40 least about 7 nucleotides long, oligos having only over about 0.02%, more preferably over about 0.1%, still more preferably over about 1%, and even more preferably over about 4% adenosine nucleotides, and up to about 30%, more preferably up to about 15%, still more preferably up to about 10% and even more preferably up to about 5%, adenosine nucleotide, or lacking adenosine altogether, and oligos in which one or more of the adenosine nucleotides have been replaced with so-called universal bases, which may pair up
- 45 with thymidine nucleotides but fail to substantially trigger adenosine receptor activity. Examples of human sequences and fragments, which are not limiting, of anti-sense oligonucleotide of the invention are the following fragments as well as shorter segments of the fragments and of the full gene or mRNA coding sequences, exons and intron-exon junctions encompassing preferably 7, 10, 15, 18 to 21, 24, 27, 30, n-1 nucleotides for each sequence, where n is the sequence's total number of nucleotides. These fragments

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may be selected from any portion of the longer oligo, for example, from the middle, 5'- end, 3'- end or starting at any other site of the original sequence. Of particular importance are fragments of low adenosine nucleotide content, that is, those fragments containing less than or about 30%, preferably less than or about 15%, more preferably less than or about 10%, and even more preferably less than or about 5%, and most preferably those devoid of adenosine nucleotide, either by choice or by replacement with a universal base in accordance with this invention. The agent of the invention includes as a most preferred group sequences and their fragments where one or more adenosines present in the sequence have been replaced by a universal base (B), as exemplified here. Similarly, also encompassed are all shorter fragments of the B-containing fragments designed by substitution of B(s) for adenosine(s) (A(s)) contained in the sequences, fragments thereof or segments thereof, as described above. A limited list of sequences and fragments is provided below.

Some of the examples of anti-sense oligonucleotide sequence fragments target the initiation codon of the respective gene, and in some cases adenosine is substituted with a universal or alternative base adenosine analogue denoted as "B", which lacks ability to bind to the adenosine A₁ and/or A₃ receptors. In fact, such replacement nucleotide acts as a "spacer". Many of the examples shown below provide one such sequence and many fragments overlapping the initiation codon, preferably wherein the number of nucleotides n is about 7, about 10, about 12, about 15, about 18, about 21 and up to about 28, about 35, about 40, about 50, about 60.

Human Receptor-related Antisense Polynucleotide

5'-GGCGGCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGCTGGG C TGCTTTTCT TTTCTGGGCC
TCTGTGGTCT GTTTTTTCT GGCCCTGCTG GGGCGCTCTC CGCCGCCCGC CTGGCTCCCG GBGCCCCBTGB
TGGGCBTGCC GTGGTTCTTG CCCTCCTTTG GCTGCCGTGC CCGCTCCCCG GCCTCCTGGC GGGTGGCCGT
TGGGCCCGTG TTCCCCTGGG GCCTGGGGCT CCCTTCTCTC GCCCTTCTTG CTGGGCCTCT GCTGCTGCTG
GTGCTGTGGC CCCCCTACA CCGAGGAGCC CATGATGGGC ATGCCACAGA CGACAGGCGT BCBCCGBGG
GCCCCBTGBTG GGCBTGCCBC BGBCBGBG C GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC
CGC GCG GGG CCC CTC CGG TCC GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC CGG GTC GGG GCC CCC
CGC GGC C GCC TCG GGG CTG GGG CGC TGG TGG CCG GG CCG CGC CTC CGC CTG CCG CTT CTG GCT GGG
CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG TCC CCG TG ACA GCG CGT CCT GTG TCT CCA GCA GCA TGG
CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT GTG TCT CCB GCB GCB TGG CCG GGC CBG CTG GGC CCC ACA
GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT
CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG CTT TCT TCT GTT CCC BCB GBG CBG TGC TGT
TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GTT GGG C TTT CTT CTG TTC
CC TTT CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT
TTC ATT AAC CGA GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT GCC
TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT
GTG G GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C GGG
TCT TGC TCT GGG CCT GGC TGT GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC TCT CTG
AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA TCT CTG BBT BTT GBC CTT CCT CCB
TGG CGG TCC TGC TTG GBT TCT CCC GB GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT ACA
GTA GAG TAG GGG ATT CCA TGG CAG GAG CCA TCT TCT TCA TGG ACT CC TTC AAG GAG ACC TTA GGT TTC
TGA GGG ACT GCT AAC ACG CCA TCT GGA GC BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT
TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GTT GTT
TTT GGG GTT TGG CTT GCC TTT CCT GGT TCT CTT BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT
TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GCC TGT
GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC CGG GCT GTG
G GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C CCC BGB BCG
BGB CCC GGB CCG BCB GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC GAT CTC TGA ATA
TTGA CCT TCC ATG GCG GTC CTG CTT GGA GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB
TCT GGG GTG TCC TGG CCT TCG TGG TTC CTC TTC CTT CGT TTG CCG TCC GCG GGG GCC CCC GGG CCT GGC
TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CC CGT GTG TTT GCG CCC TC

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CTC CTG GTC GCG CTT GTC GTT TTG GGG CCG GCT TTG CCC GCC TCC CGG CGC CTG GCC CGG CC TTC CTG
GGC TGC GTG CGC GTT CTG TTC TTC TTC CTG GCT CTG GGG TGT CCT GGC CTT CGT GGT TCC TCT TCC TTC
GTT TGC CGT CCG CGG GGG CCC CCG GGC CT GGC TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG
CTG GGG GGT GCT CCC GTG TGT TTG CGC CCT CCT CCT GGT CGC GCT TGT CGT TTT GG GGC CGG CTT TGC
5 CCG CCT CCC GGC GCC TGG CCC GGC CTT CCT GGG CTG CGT GCG CGT TCT GTT CTT CTT CCT GGC GCA GGA
GAC AGG GCA GGG CGA TCA GGA GCA GCG TGA GCC AAA GGA GGA CCA TCG GGA ACG CAG CTC CGG AAC
GCA GGA CAG AGG TGC C GC BGG BGB CBG GGC BGG GCG BTC BGG BGC BGC GTG BGC CBB BGG BGG BCC
BTC GGG BBC GCB GCT CCG GBB CGC BGG BCB GBG GTG CC TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT
CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG
10 GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC
TCC CTT CCT CTG TCT TGC CTC CTT CCT CTG GGT CCT CTT GGC CTG GGC GCT CTT CCC CTC GGG CGG CTG
CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT GCT CCT TCC CTT TCC CCG CTC GTG GGG TTT GCG
GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG GTC GGC TGG CTG CTG CTT CGG GCC GCC TGG GCT
TCC CTG TGC CCC TTT CCT CTG CTG GGT CCC CCT CCC GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA
15 GGA CAG AGC CAG GCA AGC ACC CAT GGG GAT CCA GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC
GGC GCT BCB GGB CBG BGC CBG GCB BGC BCC CBT GGG GBT CCB GGC CCB GCT G CTCAGTGGCC
CCCCAAAGGA TGAGTAATAC ATGCGCCACG ATGATCATAT CCTTTTACT ATGAGGCCGT GTCTGTCTGTG
TCTTTCCTTT GCTCTTGGTG TGTCTTTGCT GTGCCCTGCC TCTCTGCCCG TGTCTGTCTGTG GTCTTTCCTT
TGCTCTTGGT GTGTCTTTGC TGTGCCCTGC CTCTCTGCC CGTGTCTGTG GTGTCTTTCC TTTGCTCTTG
20 GTGTGTCTTT GCTGTGCCCT GCCTCTCTGC GGGGGTGGCT TCCTGCCGCG TCTCTGGGCC GTCCCGTCCC
TCGGCCCCGC GCCGCGCTCG GCTCCTCTCC CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC
GGCGCTGCC TGCGCGCGGC GCTGGCCCT GCTGGCCGTC GGCTGCGCGC TGCTGGCTGC CCTGCTGGCC
GCGCCGGGGC CTGTCCGCT CTGCGGGCGC TGTCTCTGG CTTGTCTTCC GGCTCTTCTG CTGGGGTGGG
GCTGGGCGGC CGGCCCGGTG CTGGGGCTCC TCGGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGGC
25 GGGGGTTTCT GGCCGTGGGG GTCTTGCTG GCCTCCGGGC TCCTGCTTGT CTGCTTCTC TTCTCTGGTC
GGTGTGGCT CGGGGCTCCG TGGGTCCCTG GCGCCCGTT GTGTTTTGTC TTTTCCCTG GCGTCCCTGT
GCCCCCTCTC TCTCCTTCT CTGCTTCTG CTCTCCTTTG TGGGGCCCTC CCTGCTGTCT TTGGTTTTGG
GCTTTTTTTC TCTTCTCCT TTTTCGTGCG TGGGCTCC GCACGCTCT TGCCACCTCC TGCGCAGGGC
AGCGCCTTGG GGCCAGCGCC GCTCCCGCG CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG
30 CATGCTTCT CCTCGGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC GCBCGCCTC TTGCCBCTC
CTGCGCBGGG CBGCGCCTT GGGCCBGC GCCTCCCGGC GCGGCCBGC BGGCBGCCBG CBGCGCGCBG
CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB GCGGBCBGG C GCTGCCCGGC
GGGGTGTGCG CTTGGCGCTC CCGTGCTCG TTCTCTGTCT CCCGTTCCC CTTGCTGGC GTCTCGGGCC
TTCGCTCTCT TCCTCTCTT CCTTCCGCTC CGTGGGGGCT GCTTGGTGGG GGCCTGTGCT CGGGGTCCC
35 GGGCTTCTGG CCCTTGCCGT TCATGGTGGC TAGGTGGGG GTTCBTGGTG GCTBGGTGG GC GGG GTG GGT
BGG CCG TGT CTG GGGGT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT TGG CTT TCT
TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT
TGGCG CTG GCG GGG GGG CCT CTGCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGGTGG CGG GCG
TGG TGG CCT CTG TGGGG CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCTT TGC GCT CCC GGG CCG
40 CCGGG GTG GGT AGG CCG TGT CTG GGGGT GGC CAT GTT GGT TGC CCGG CCC GCG GCT GCA GGG G
ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTAGATC ATCAAAATCC CACATCTGTG
GATCTGTAAT ATTTGACATG TCCTCTTCTAG TTTCAGCAAT GGTGTGATCT AACTGAAGCA CCGGCCAGGB
CBGGGGCTGT BBTCTTCTC TGCBBGTGGC BTGCCBGTGB BBTBTBGTB BTCTBBBTCC CBCBTCTGTG
GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBG BCCGGCCBGG
45 TGGCTCGGTG CTTCTGCCCC TGTGTTGCG GCGCTCGGT GGTGTGGCC CTGTGGTGTCT TCGTTTCCCC
CTCTTCTCT TTGTTGCGGG GTTCTTGTGG CGGCTGCTT GTCTCGTTCC GCCCTGTCC GCGGGAAGCC
TCTCTCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA ACCAGGGCGC GTCCGCACAG
ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC GCGCGCC CTGTGCGGGC
GGBBGCTCT CTCCTCTCCC CBGBTCCGCG BCBGGCCGCB GGCBBGBBCC BGCGCBCCB GGGCGCGTCC
50 GCBCBGBCTT GGBGGCGGCT GCBTGCTGCT BCCTGCTCGGGCG GGBBGCTCCG GTGGCCGCCG CGCGTCCGGT
GGCCGCCGCG CCTCTCTCT CTCCCCTGG CCCTGTCGGG CGGGTCTCT CGTCTGTCT CTTTTCTTT
TGCTGTCTT TCTTCCCGTC TCTGCTTT GTCTGTCTC CCCGTCTCT CCCACTGCT CTCCCGGGG

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CTTCCCCGGC TTCGGGTGGC CGGTGTCCCG GGCTCCGGCG CGGCGGCGGC TTCGGCTGCG GGTGGGTGGC
GCGGGCTGCC GGGTCCGCGC GCGCCTGGG CCCTTGTGCT GCTTTTGTCT TGTTCGGTTC TGGCTGCTCC
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5 CGGGTGGCCG GTGTCCCGGG CTCCGGCGCG GCGGCGGCTT CGGCTGCGGG TGGGTGGCGC GGGCTGCCCG
GTCCGCGCGG CGCCTGGGCC CTGTGCTGC TTTTGTGCTT TCCGTTCTG GCTGCTCCGG TCTGTGTTGT
GGTTGTTTTG TTTCTTCTG GGTGTGGGCC TTGCGGTTTT GGCTGTGGGC CCTTGGGGC CTGGCTTCT
GGCTCCAT CCACATGATT GCTTAGATT GTGCTGTATC TCTCAGGATT ATCACTGATT ACACATCCAA
CCAGTGCCAG CCAAAAGGAT GCCCTGAGGC AAAGGGTTT CATCTTGAGG CAAATTTAG GACBTCCBC
10 BTGBTTGCTT BGBTTGTGC TGTBTCTCTC BGGBTBTBC CTGBTTBCBC BTCCBBCCBG TGCCBGCCBB
BBGGBTGCC TGBGGCBBG GGTTCBCTC TTGBGGCBBB TTTGBGGGGGCTBBGBT GBTCCBCBCTC BCTBCCBCGT
TGCCCBCCBC BGBGTBCC BCBBTGBCG TGTBGGCBGC TGCCBBBGG BCBBTTTGCC BGGCTGGTTG
CBCGBBCTGB TTGGGTTCCG BGGTGTBTGT GGBGTGTTT GGGGBGBGGT CTGBGTCCBC CGGGBGGBCG
TTBTCCBT TCBGGCTBGG CGGTBBBGCC CTBCTBTCTG TBCBCBBCC CCTCTGCBG CBGBGTCTG
15 TCGTGGCGCC TGGGGCTCBG GGTCCGGGC TAAGATGATC CACATCACTA CCACGTTGCC CACCACAGAG
GTCACCACAA TGACCGTGTA GGCAGCTGCC CAAAGGACAA TTTGCCAGGC TGGTTGCACG AACTGATTGG
GTTCCGAGGT GTTAGTGAG ATGTTTGGGG AGAGGTCTGA GTCCACCGGG AGGACGTTAT CCATTTCGAA
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20 TCTCTGTGTT TGCTGCCCTG GGTCTGGGGG TGTGGCCTTG GGGCCGTCCT CTGGCTCCTC CTCGTGGGCC CCC
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CGGGTGGCCA GCACGAACAG CACCCAGAGG AAGGGGGGCG GCGCAGAAGG GCAGCCCGCA GGCCAGGATC
AGGTCTGCTG CGGCCGAGA TAATGGCATT CACCACGCGG CGGCCAGCG CACGCCGCGC ATCCGGCCCG
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25 CTGGGGCAGG GACGGGGTG BCBTTGBGCB TGTGCGCGCG GTCCCGTTBB GBGTGGGGCC GCCAGCCAG
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CCCGCAGGCC AGGATCAGGT CTGCTGCGGC CGGAGATAAT GGCATTACC ACGCGGCGG CCAGCGCACG
CCGCGCATCC GGCCCGGGT CTGACCTGCA GCGCCGCTCT CCTTGGCATT CTGGGCCCC AGTCACTCCT
CTCCCTGCC CCCTTGCTGG GGCAGGGACG GCGTGTGT CBGTGGTGCT GCGCGTTGB GGTBTGGCGC
30 TCCBCCBTT CCCTTTCTC CTGTTTTCC GTTCTCTTG CCGTCTGTGG TT ATGCCGCCCT CCATCTCAGC
TTTCCAGGCC GCCTACATCG GCATCGAGGT GTCATCGCC CTGGTCTCTG TGCCCGGAA CGTGCTGGTG
ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTCTCG CTGGCGGTGG
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CCACACCTGC CTCATGGTTG CCGTCCGGT CCTCATCTC ACCCAGAGCT CCATCCTGGC CTGCTGGCA
35 ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCGCGAGGG
CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCTG GGTGGGACTG CCCCTATGT TTGGCTGGAA
CAATCTGAGT GCGGTGGAGC GGGCCTGGG AGCCAACGGC AGCATGGGG AGCCCGTGAT CAAGTGCAG
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40 CTCCTCCGGC GACCCGAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCTC
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ACAAGCCAG CATCCTTACC TACATTGCCA TCTCCTCAC GCACGGCAAC TCGGCCATGA ACCCATTTGT
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45 GGTGCTGTG TCTGAATCCC AGAGCCTCCT CTCCTCTGT GAGGCTGGCA GGTGAGGAAG GGTAAACCT
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TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG CCGGGCTGGG AGCGCTGCGG CGGGAGCCGG
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50 CTTGGTGCC GTCTGCTGAT GTGCCAGCC TGTGCCGCG ATGCCGCCCT CCATCTCAGC TTTCCAGGCC
GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGAA CGTGCTGGTG ATCTGGGCGG
TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTGTG CTGGCGGTGG CTGATGTGGC

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CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC
CTCATGGTTG CCTGTCCGGT CCTCATCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG
ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCAGAGGG CGGCGGTGGC
CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT
5 GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG
TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT
CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC
GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC CCTCATCTC TTCCTCTTG
CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTG CCGTCTGCC ACAAGCCCAG
10 CATCCTTACC TACATTGCCA TCTTCTCAC GCACGGCAAC TCGGCCATGA ACCCCATTGT CTATGCCTTC
CGCATCCAGA AGTTCGCGT CACCTTCCTT AAGATTGGGA ATGACCATTT CCGTGCCAG CCTGCACCTC
CCATTGACGA GGATCTCCA GAAGAGAGGC CTGATGACTA GACCCCGCCT TCCGCTCCA CCAGCCCACA
TCCAGTGGGG TCTCAGTCCA GTCTCACAT GCCCGCTGTC CCAGGGGTCT CCCTGAGCCT GCCCCAGCTG
GGCTGTTGGC TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT GTGGTCCCTC CACTAGGAGT
15 TAACTACCTT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT CCTACGGAGG GACCAGGTGT
CTAGAGGCAA CAGTGTCTG AGCCCCACC TGCCTGACCA TCCCATGAGC AGTCCAGCGC TTCAGGGCTG
GGCAGGTCCT GGGGAGGCTG AGACTGCAGA GGAGCCACCT GGGCTGGGAG AAGGTGCTTG GGCTTCTGCG
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AGCATCTGCT CTGAGACGGA TGGAAGGAGA GAGGTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG
20 GCCAGAGGCA GCTAAGGGGC AGGAATCAAG GAGCCTCGT TCCCACCTCT GAGGACTCTG GACCCAGGC
CATAACAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA TTGTACGTGG GAGAGGCAGA
AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC ACGCCCTGGG GAGTGAGCTT
GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA GCTCTGAGCC CTCCTTCTTG CCCTGAGCTT
TCCGGGGAGG AGCCTGGAGT GTAATTACCT GTCATCTGGG CCACCAGCTC CACTGGCCCC CGTTGCCGGG
25 CCTGGACTGT CCTAGGTGAC CCCATCTCTG CTGCTTCTGG GCCTGATGGA GAGGAGAACA CTAGACATGC
CAACTCGGGA GCATTCTGCC TGCCTGGGAA CGGGGTGGAC GAGGGAGTGT CTGTAAGGAC TCAGTGTGTA
CTGTAGGCGC CCCTGGGGTG GGTTTAGCAG GCTGCAGCAG GCAGAGGAGG AGTACCCCC TGAGAGCATG
TGGGGGAAGG CCTTGCTGTC ATGTGAATCC CTCAATACCC CTAGTATCTG GCTGGGTTTT CAGGGGCTTT
GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT AGGACTTTAG GGATCTGGGA TCTGGGGAAG GACCAACCCA
30 TGCCCTGCCA AGCCTGGAGC CCCTGTGTTG GGGGGCAAGG TGGGGGAGCC TGGAGCCCCT GTGTGGGAGG
GCGAGGCGGG GGAGCCTGGA GCCCCTGTGT GGGAGGGCGA GCGGGGGGAT CCTGGAGCCC CTGTGTCGGG
GGGCGAGGGA GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGTG AACTCCAGGA CTTGCTTCCA
AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC CCATGTGACT AATAAAAAAC
TGTGAACCTT CGCATTTGTG TTTAATAAAA AGAATCTGGA AGATAAATAG TCTTGAAGAG AGACAAAGGA
35 AGGAAAATTT AAATCCTTAG ATTCAGCAG AAGAATTCCA TGTGGAAGGT TTGGGTGTGT GTTGTGTGTG
TTTGGTGTGT TTTTGTGTTT TTTGTTTTT TGTTTTTTTT TGAGATGGAG TCTCGCTGTG TTACCGGGAG
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						ATG	

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	TCTACTAAAA	ATACAAAAAA	AAAATTAGCT	GGGTGTGGTG	GCAGTCACCT	GTAGTCCCAG	CTACTTGGGA

Figure 1 consists of 12 bar charts, each representing a different variable. The x-axis for all charts lists four groups: All respondents, Nonusers, Users, and Users who have used the program for 1 year or more. The y-axis represents the percentage of respondents, ranging from 0% to 100%.

- Age:** Shows the distribution of age groups (18-24, 25-34, 35-44, 45-54, 55-64, 65+).
- Sex:** Shows the percentage of males and females.
- Education:** Shows the percentage of respondents with different levels of education (High school or less, Some college, Bachelor's degree, Master's degree, Doctorate).
- Income:** Shows the percentage of respondents in different income brackets (\$0-\$14,999, \$15,000-\$24,999, \$25,000-\$34,999, \$35,000-\$44,999, \$45,000-\$54,999, \$55,000-\$64,999, \$65,000-\$74,999, \$75,000-\$84,999, \$85,000-\$94,999, \$95,000-\$104,999, \$105,000-\$114,999, \$115,000-\$124,999, \$125,000-\$134,999, \$135,000-\$144,999, \$145,000-\$154,999, \$155,000-\$164,999, \$165,000-\$174,999, \$175,000-\$184,999, \$185,000-\$194,999, \$195,000-\$204,999, \$205,000-\$214,999, \$215,000-\$224,999, \$225,000-\$234,999, \$235,000-\$244,999, \$245,000-\$254,999, \$255,000-\$264,999, \$265,000-\$274,999, \$275,000-\$284,999, \$285,000-\$294,999, \$295,000-\$304,999, \$305,000-\$314,999, \$315,000-\$324,999, \$325,000-\$334,999, \$335,000-\$344,999, \$345,000-\$354,999, \$355,000-\$364,999, \$365,000-\$374,999, \$375,000-\$384,999, \$385,000-\$394,999, \$395,000-\$404,999, \$405,000-\$414,999, \$415,000-\$424,999, \$425,000-\$434,999, \$435,000-\$444,999, \$445,000-\$454,999, \$455,000-\$464,999, \$465,000-\$474,999, \$475,000-\$484,999, \$485,000-\$494,999, \$495,000-\$504,999, \$505,000-\$514,999, \$515,000-\$524,999, \$525,000-\$534,999, \$535,000-\$544,999, \$545,000-\$554,999, \$555,000-\$564,999, \$565,000-\$574,999, \$575,000-\$584,999, \$585,000-\$594,999, \$595,000-\$604,999, \$605,000-\$614,999, \$615,000-\$624,999, \$625,000-\$634,999, \$635,000-\$644,999, \$645,000-\$654,999, \$655,000-\$664,999, \$665,000-\$674,999, \$675,000-\$684,999, \$685,000-\$694,999, \$695,000-\$704,999, \$705,000-\$714,999, \$715,000-\$724,999, \$725,000-\$734,999, \$735,000-\$744,999, \$745,000-\$754,999, \$755,000-\$764,999, \$765,000-\$774,999, \$775,000-\$784,999, \$785,000-\$794,999, \$795,000-\$804,999, \$805,000-\$814,999, \$815,000-\$824,999, \$825,000-\$834,999, \$835,000-\$844,999, \$845,000-\$854,999, \$855,000-\$864,999, \$865,000-\$874,999, \$875,000-\$884,999, \$885,000-\$894,999, \$895,000-\$904,999, \$905,000-\$914,999, \$915,000-\$924,999, \$925,000-\$934,999, \$935,000-\$944,999, \$945,000-\$954,999, \$955,000-\$964,999, \$965,000-\$974,999, \$975,000-\$984,999, \$985,000-\$994,999, \$995,000-\$1,004,999, \$1,005,000-\$1,014,999, \$1,015,000-\$1,024,999, \$1,025,000-\$1,034,999, \$1,035,000-\$1,044,999, \$1,045,000-\$1,054,999, \$1,055,000-\$1,064,999, \$1,065,000-\$1,074,999, \$1,075,000-\$1,084,999, \$1,085,000-\$1,094,999, \$1,095,000-\$1,104,999, \$1,105,000-\$1,114,999, \$1,115,000-\$1,124,999, \$1,125,000-\$1,134,999, \$1,135,000-\$1,144,999, \$1,145,000-\$1,154,999, \$1,155,000-\$1,164,999, \$1,165,000-\$1,174,999, \$1,175,000-\$1,184,999, \$1,185,000-\$1,194,999, \$1,195,000-\$1,204,999, \$1,205,000-\$1,214,999, \$1,215,000-\$1,224,999, \$1,225,000-\$1,234,999, \$1,235,000-\$1,244,999, \$1,245,000-\$1,254,999, \$1,255,000-\$1,264,999, \$1,265,000-\$1,274,999, \$1,275,000-\$1,284,999, \$1,285,000-\$1,294,999, \$1,295,000-\$1,304,999, \$1,305,000-\$1,314,999, \$1,315,000-\$1,324,999, \$1,325,000-\$1,334,999, \$1,335,000-\$1,344,999, \$1,345,000-\$1,354,999, \$1,355,000-\$1,364,999, \$1,365,000-\$1,374,999, \$1,375,000-\$1,384,999, \$1,385,000-\$1,394,999, \$1,395,000-\$1,404,999, \$1,405,000-\$1,414,999, \$1,415,000-\$1,424,999, \$1,425,000-\$1,434,999, \$1,435,000-\$1,444,999, \$1,445,000-\$1,454,999, \$1,455,000-\$1,464,999, \$1,465,000-\$1,474,999, \$1,475,000-\$1,484,999, \$1,485,000-\$1,494,999, \$1,495,000-\$1,504,999, \$1,505,000-\$1,514,999, \$1,515,000-\$1,524,999, \$1,525,000-\$1,534,999, \$1,535,000-\$1,544,999, \$1,545,000-\$1,554,999, \$1,555,000-\$1,564,999, \$1,565,000-\$1,574,999, \$1,575,000-\$1,584,999, \$1,585,000-\$1,594,999, \$1,595,000-\$1,604,999, \$1,605,000-\$1,614,999, \$1,615,000-\$1,624,999, \$1,625,000-\$1,634,999, \$1,635,000-\$1,644,999, \$1,645,000-\$1,654,999, \$1,655,000-\$1,664,999, \$1,665,000-\$1,674,999, \$1,675,000-\$1,684,999, \$1,685,000-\$1,694,999, \$1,695,000-\$1,704,999, \$1,705,000-\$1,714,999, \$1,715,000-\$1,724,999, \$1,725,000-\$1,734,999, \$1,735,000-\$1,744,999, \$1,745,000-\$1,754,999, \$1,755,000-\$1,764,999, \$1,765,000-\$1,774,999, \$1,775,000-\$1,784,999, \$1,785,000-\$1,794,999, \$1,795,000-\$1,804,999, \$1,805,000-\$1,814,999, \$1,815,000-\$1,824,999, \$1,825,000-\$1,834,999, \$1,835,000-\$1,844,999, \$1,845,000-\$1,854,999, \$1,855,000-\$1,864,999, \$1,865,000-\$1,874,999, \$1,875,000-\$1,884,999, \$1,885,000-\$1,894,999, \$1,895,000-\$1,904,999, \$1,905,000-\$1,914,999, \$1,915,000-\$1,924,999, \$1,925,000-\$1,934,999, \$1,935,000-\$1,944,999, \$1,945,000-\$1,954,999, \$1,955,000-\$1,964,999, \$1,965,000-\$1,974,999, \$1,

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40 Human Enzyme-related Antisense Polynucleotide

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3	0.98	0.99	1.00	0.99	0.98	0.97	0.96	0.95	0.94	0.93	0.92	0.91	0.90	0.89	0.88	0.87	0.86	0.85	0.84	0.83	0.82	0.81	0.80	0.79	0.78	0.77	0.76	0.75	0.74	0.73	0.72	0.71	0.70	0.69	0.68	0.67	0.66	0.65	0.64	0.63	0.62	0.61	0.60	0.59	0.58	0.57	0.56	0.55	0.54	0.53	0.52	0.51	0.50	0.49	0.48	0.47	0.46	0.45	0.44	0.43	0.42	0.41	0.40	0.39	0.38	0.37	0.36	0.35	0.34	0.33	0.32	0.31	0.30	0.29	0.28	0.27	0.26	0.25	0.24	0.23	0.22	0.21	0.20	0.19	0.18	0.17	0.16	0.15	0.14	0.13	0.12	0.11	0.10	0.09	0.08	0.07	0.06	0.05	0.04	0.03	0.02	0.01	0.00
4	0.97	0.98	0.99	1.00	0.99	0.98	0.97	0.96	0.95	0.94	0.93	0.92	0.91	0.90	0.89	0.88	0.																																																																																						

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Human Adenosine A₁ Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

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45 TCCTCAGCA CGGCAACTCG GCCATGAACC CCATTGTCTA TGCTTCCGC ATCCAGAAGT TCCGCGTCAC
CTTCCTAAG ATTTGGAATG ACCATTTCCG CTGCCAGCCT GCACCTCCA TTGACGAGGA TCTCCAGAA
GAGAGGCCTG ATGACTAGAC CCCGCCCTCC GCTCCCACCC CCCACATCCA GTGGGGTCTC AGTCCAGTCC
TCACATGCCC GCTGTCCCAG GGTCTCCCT GAGCTGGGCT CAGCTGGGCT GTTGGCTGGG GGCATGGGGG
AGGCTCTGAA GAGATACCA CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCCC
50 TGCAGGAGGC CTGGGAGGGC AAGGGTCTCA CGGAGGGACC AGGTGTCTAG AGGCAACAGT GTTCTGAGCC
CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGGCA GGTCTGGGG AGGCTGAGAC
TGCAGAGGAG CCACCTGGGC TGGGAGAAGG TGCTTGGGCT TCTGCGGTGA GGCAGGGGAG TCTGCTGTG
TTAGATGTTG GTGGTGCAGC CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA
AGGAGAGAGG TTGAGGATGC ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA -3'
55 (FRAG. NO: 2422)(SEQ. ID NO: 2422)
5'-ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT CTCCTCTGT GAGGCTGGCA
GGTGAGGAAG GGTTTAACCT CACTGGAAGG AATCCCTGGA GCTAGCGGCT GCTGAAGGCG TCGAGGTGTG
GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG CCGGGCTGGG
AGCGTGC GG GAGCCGG AGGACTATGA GCTGCCGCGC GTTGTCCAGA GCCCAGCCCA GCCCTACGCG
60 CGCGGCCCGG AGCTCTGTTC CCTGGAACCT TGGGCACTGC CTCTGGGACC CCGCCGGCC AGCAGGCAGG
ATGGTGCTTG CCTCGTGCCC CTGGTGCCC GTCTGCTGAT GTGCCAGCC TGTGCCGCC ATGCCGCCCT

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CCATCTCAGC TTTCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA
CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT CATCGTGTCTG
CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC
AGACCTACTT CCACACCTGC CTCATGGTTG CCGGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC
5 CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT GGTGGTGACC
CCCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT TCTCCTTCGT AGCCCTATGT
TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG AGCCCGTGAT
CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG
CCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA
10 AGGTGTCGGC CTCCTCCGGC GACCCGAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA AGTCGCTGGC
CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC
CCGTCCTGCC ACAAGCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA
ACCCATTGT CTATGCCTTC CGCATCCAGA AGTTCGCGCT CACCTTCCTT AAGATTGGA ATGACCATT
CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA GACCCCGCCT
15 TCCGCTCCCA CCAGCCACA TCCAGTGGG TCTCAGTCCA GTCTCACAT GCGCGCTGTC CCAGGGGTCT
CCCTGAGCCT GCGCCAGCTG GGCTGTTGGC TGGGAGGCTG GGGGAGGCTC TGAAGAGATA CCCACAGAGT
GTGGTCCCTC CACTAGGAGT TAACTACCCT ACACCTCTGG GCCCTGCAGG AGCCCTGGGA GGGCAAGGGT
CCTACGAGG GACCAGGTGT CTAGAGGCAA CAGTGTCTG AGCCCCACC TGCCTGACCA TCCCATGAGC
AGTCCAGCGC TTCAGGGCTG GGCAGGTCTT GGGGAGGCTG AGACTGCAGA GGAGCCACCT GGGCTGGGAG
20 AAGGTGCTTG GGCTTCTCGG GTGAGGCAGG GGAGTCTGCT TGTCTTAGAT GTTGGTGGTG CAGCCCCAGG
ACCAAGCTTA AGGAGAGGAG AGCATCTGCT CTGAGACGGA TGGAAGGAGA GAGGTTGAGG ATGCACTGGC
CTGTTCTGTA GGAGAGACTG GCCAGAGGCA GCTAAGGGGC AGGAATCAAG GAGCCTCCGT TCCCACCTCT
GAGGACTCTG GACCCAGGC CATAACAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA
TTGTACGTGG GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC
25 ACGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA CGAGGTGGTA GCTCTGAGCC
CTCCTTCTTG CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT GTAATTACCT GTCATCTGGG CCACGAGCTC
CACTGGCCCC CGTTGCCGGG CCTGGACTGT CCTAGGTGAC CCCATCTCTG CTGCTTCTGG GCCTGATGGA
GAGGAGAAC CTAGACATGC CAACTCGGGA GCATTCTGCC TGCTGGGAA CGGGGTGGAC GAGGGAGTGT
CTGTAAGGAC TCAGTGTGA CTGTAGGCGC CCCTGGGGTG GGTTAGCAG GCTGCAGCAG CAGAGGAGG
30 AGTACCCCC TGAGAGCATG TGGGGGAAGG CCTTGCTGTC ATGTGAATCC CTCAATACCC CTAGTATCTG
GCTGGGTTT CAGGGGCTT GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT AGGACTTTAG GGATCTGGGA
TCTGGGGAAG GACCAACCCA TGCCCTGCCA AGCCTGGAGC CCCTGTGTTG GGGGGCAAGG TGGGGGAGCC
TGGAGCCCC GTGTGGGAGG GCGAGGCGGG GGAGCCTGGA GCCCTGTGT GGGAGGGCGA GCGGGGGGAT
CCTGGAGCCC CTGTGTCGGG GGGCGAGGGA GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGTC
35 AACTCCAGGA CTTGCTTCCA AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC
CCATGTGACT AATAAAAAAC TGTGAACCCT -3' (FRAG. NO:) (SEQ. ID NO: 2421)
5'-ATGCCGCCCT CCATCTCAGC TTTCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG
TGCCCGGGAA CGTGCTGGTG ATCTGGGCGG TGAAGGTGAA CCAGGCGCTG CGGGATGCCA CCTTCTGCTT
CATCGTCTCG CTGGCGGTGG CTGATGTGGC CTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC
40 ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCGGTCCGGT CCTCATCCTC ACCCAGAGCT
CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT
GGTGGTGACC CCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT TCTCCTTCGT GGTGGGACTG
CCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGGG
AGCCCGTGAT CAAGTGCGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT
45 GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG
CTCAACAAGA AGGTGTCGGC CTCCTCCGGC GACCCGAGA AGTACTATGG GAAGGAGCTG AAGATCGCCA
AGTCGCTGGC CCTCATCCTC TTCCTCTTTG CCCTCAGCTG GCTGCCTTTG CACATCCTCA ACTGCATCAC
CCTCTTCTGC CCGTCTGCC ACAAGCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC
TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCGCGT CACCTTCCTT AAGATTGGA
50 ATGACCATT CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA GAAGAGAGGC CTGATGACTA G
(FRAG NO:) (SEQ. ID NO: 2420)
5'-GAT GGA GGG CGG CAT GGC GGG-3' (FRAG. NO: 1657) (SEQ ID NO:2412)
5'-G CGG GTC GCC GG-3' (FRAG. NO: 1658) (SEQ ID NO:2413)
5'-GGC GGG CBC BGG C-3' (FRAG. NO: 1659) (SEQ ID NO:2414)
55 5'-GGC GGG CBC-3' (FRAG. NO: 1660) (SEQ ID NO:2415)
5'-GC GGC CTG G-3' (FRAG. NO: 1661) (SEQ ID NO:2416)
5'-GGB GGG CGG C-3' (FRAG. NO: 1662) (SEQ ID NO:2417)
5'-GBT GGB GGG-3' (FRAG. NO: 1663) (SEQ ID NO:2418)
5'-GG CTG GGC-3' (FRAG. NO: 1664) (SEQ ID NO:2419)
60 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG.1) (SEQ. ID NO: 11)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 2) (SEQ. ID NO:12)

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- 5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 3) (SEQ. ID NO: 13)
5'-GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 4) (SEQ. ID NO: 14)
5'-C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 5) (SEQ. ID NO: 15)
5'-CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 6) (SEQ. ID NO: 16)
5 5'-TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 7) (SEQ. ID NO: 17)
5'-G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 8) (SEQ. ID NO: 18)
5'-GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 9) (SEQ. ID NO: 19)
5'-AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 10) (SEQ. ID NO: 20)
5'-A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 11) (SEQ. ID NO: 21)
10 5'-AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 12) (SEQ. ID NO: 22)
5'-GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 13) (SEQ. ID NO: 23)
5'-C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 14) (SEQ. ID NO: 24)
5'-TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 15) (SEQ. ID NO: 25)
5'-GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 16) (SEQ. ID NO: 26)
15 5'-A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 17) (SEQ. ID NO: 27)
5'-GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 18) (SEQ. ID NO: 28)
5'-AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 19) (SEQ. ID NO: 29)
5'-T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 20) (SEQ. ID NO: 30)
5'-GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 21) (SEQ. ID NO: 31)
20 5'-GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 22) (SEQ. ID NO: 32)
5'-A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 23) (SEQ. ID NO: 33)
5'-GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 24) (SEQ. ID NO: 34)
5'-GG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 25) (SEQ. ID NO: 35)
5'-G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 26) (SEQ. ID NO: 36)
25 5'-CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 27) (SEQ. ID NO: 37)
5'-GG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 28) (SEQ. ID NO: 38)
5'-G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 29) (SEQ. ID NO: 39)
5'-CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 30) (SEQ. ID NO: 40)
5'-AT GGC GGG CAC AGG CTG GGC-3' (FRAG 31) (SEQ. ID NO: 41)
30 5'-T GGC GGG CAC AGG CTG GGC-3' (FRAG 32) (SEQ. ID NO: 42)
5'-GGC GGG CAC AGG CTG GGC-3' (FRAG 33) (SEQ. ID NO: 43)
5'-GC GGG CAC AGG CTG GGC-3' (FRAG 34) (SEQ. ID NO: 44)
5'-C GGG CAC AGG CTG GGC-3' (FRAG 35) (SEQ. ID NO: 45)
5'-GGG CAC AGG CTG GGC-3' (FRAG 36) (SEQ. ID NO: 46)
35 5'-GG CAC AGG CTG GGC-3' (FRAG 37) (SEQ. ID NO: 47)
5'-G CAC AGG CTG GGC-3' (FRAG 38) (SEQ. ID NO: 48)
5'-CAC AGG CTG GGC-3' (FRAG 39) (SEQ. ID NO: 49)
5'-AC AGG CTG GGC-3' (FRAG 40) (SEQ. ID NO: 50)
5'-C AGG CTG GGC-3' (FRAG 41) (SEQ. ID NO: 51)
40 5'-AGG CTG GGC-3' (FRAG 42) (SEQ. ID NO: 52)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 43) (SEQ. ID NO: 53)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 44) (SEQ. ID NO: 54)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 45) (SEQ. ID NO: 55)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 46) (SEQ. ID NO: 56)
45 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 47) (SEQ. ID NO: 57)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC AGG CT-3' (FRAG 48) (SEQ. ID NO: 58)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 49) (SEQ. ID NO: 59)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 50) (SEQ. ID NO: 60)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 51) (SEQ. ID NO: 61)
50 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CAC-3' (FRAG 52) (SEQ. ID NO: 62)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG CA-3' (FRAG 53) (SEQ. ID NO: 63)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG C-3' (FRAG 54) (SEQ. ID NO: 64)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGG -3' (FRAG 55) (SEQ. ID NO: 65)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GG-3' (FRAG 56) (SEQ. ID NO: 66)
55 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC G-3' (FRAG 57) (SEQ. ID NO: 67)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC -3' (FRAG 58) (SEQ. ID NO: 68)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TG -3' (FRAG 59) (SEQ. ID NO: 69)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT T-3' (FRAG 60) (SEQ. ID NO: 70)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 61) (SEQ. ID NO: 71)
60 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 62) (SEQ. ID NO: 72)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 63) (SEQ. ID NO: 73)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 64) (SEQ. ID NO: 74)

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- 5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 65) (SEQ. ID NO: 75)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 66) (SEQ. ID NO: 76)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 67) (SEQ. ID NO: 77)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 68) (SEQ. ID NO: 78)
5 5'-GGC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 69) (SEQ. ID NO: 79)
5'-GGC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 70) (SEQ. ID NO: 80)
5'-GGC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 71) (SEQ. ID NO: 81)
5'-GGC GGC CTG GAA AGC TGA GAT G -3' (FRAG 72) (SEQ. ID NO: 82)
5'-GGC GGC CTG GAA AGC TGA GAT -3' (FRAG 73) (SEQ. ID NO: 83)
10 5'-GGC GGC CTG GAA AGC TGA GA-3' (FRAG 74) (SEQ. ID NO: 84)
5'-GGC GGC CTG GAA AGC TGA G-3' (FRAG 75) (SEQ. ID NO: 85)
5'-GGC GGC CTG GAA AGC TGA-3' (FRAG 76) (SEQ. ID NO: 86)
5'-GGC GGC CTG GAA AGC TG-3' (FRAG 77) (SEQ. ID NO: 87)
5'-GGC GGC CTG GAA AGC T-3' (FRAG 78) (SEQ. ID NO: 88)
15 5'-GGC GGC CTG GAA AGC-3' (FRAG 79) (SEQ. ID NO: 89)
5'-GGC GGC CTG GAA AG-3' (FRAG 80) (SEQ. ID NO: 90)
5'-GGC GGC CTG GAA A-3' (FRAG 81) (SEQ. ID NO: 91)
5'-GGC GGC CTG GAA-3' (FRAG 82) (SEQ. ID NO: 92)
5'-GGC GGC CTG GA-3' (FRAG 83) (SEQ. ID NO: 93)
20 5'-GGC GGC CTG G-3' (FRAG 84) (SEQ. ID NO: 94)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG GGC-3' (FRAG 85) (SEQ. ID NO: 95)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG GG-3' (FRAG 86) (SEQ. ID NO: 96)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG G-3' (FRAG 87) (SEQ. ID NO: 97)
25 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CTG -3' (FRAG 88) (SEQ. ID NO: 98)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG CT-3' (FRAG 89) (SEQ. ID NO: 99)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG C-3' (FRAG 90) (SEQ. ID NO: 100)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC AGG -3' (FRAG 91) (SEQ. ID NO: 101)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGC CAC AG-3' (FRAG 92) (SEQ. ID NO: 102)
30 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC A-3' (FRAG 93) (SEQ. ID NO: 103)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGC CAC-3' (FRAG 94) (SEQ. ID NO: 104)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGC CA-3' (FRAG 95) (SEQ. ID NO: 105)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGC C-3' (FRAG 96) (SEQ. ID NO: 106)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GGC -3' (FRAG 97) (SEQ. ID NO: 107)
35 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC GG-3' (FRAG 98) (SEQ. ID NO: 108)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC G-3' (FRAG 99) (SEQ. ID NO: 109)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT TGC -3' (FRAG 100) (SEQ. ID NO: 110)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 101) (SEQ. ID NO: 111)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 102) (SEQ. ID NO: 112)
40 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 103) (SEQ. ID NO: 113)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 104) (SEQ. ID NO: 114)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 105) (SEQ. ID NO: 115)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 106) (SEQ. ID NO: 116)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 107) (SEQ. ID NO: 117)
45 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 108) (SEQ. ID NO: 118)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 109) (SEQ. ID NO: 119)
5'-GC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 110) (SEQ. ID NO: 120)
5'-GC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 111) (SEQ. ID NO: 121)
5'-GC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 112) (SEQ. ID NO: 122)
50 5'-GC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 113) (SEQ. ID NO: 123)
5'-GC GGC CTG GAA AGC TGA GAT G -3' (FRAG 114) (SEQ. ID NO: 124)
5'-GC GGC CTG GAA AGC TGA GAT -3' (FRAG 115) (SEQ. ID NO: 125)
5'-GC GGC CTG GAA AGC TGA GA-3' (FRAG 116) (SEQ. ID NO: 126)
5'-GC GGC CTG GAA AGC TGA G-3' (FRAG 117) (SEQ. ID NO: 127)
55 5'-GC GGC CTG GAA AGC TGA-3' (FRAG 118) (SEQ. ID NO: 128)
5'-GC GGC CTG GAA AGC TG-3' (FRAG 119) (SEQ. ID NO: 129)
5'-GC GGC CTG GAA AGC T-3' (FRAG 120) (SEQ. ID NO: 130)
5'-GC GGC CTG GAA AGC-3' (FRAG 121) (SEQ. ID NO: 131)
5'-GC GGC CTG GAA AG-3' (FRAG 122) (SEQ. ID NO: 132)
60 5'-GC GGC CTG GAA A-3' (FRAG 123) (SEQ. ID NO: 133)
5'-GC GGC CTG GAA-3' (FRAG 124) (SEQ. ID NO: 134)
5'-GC GGC CTG GA-3' (FRAG 125) (SEQ. ID NO: 135)

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5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 126) (SEQ. ID NO: 136)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 127) (SEQ. ID NO: 137)
5 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 128) (SEQ. ID NO: 138)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 129) (SEQ. ID NO: 139)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 130) (SEQ. ID NO: 140)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 131) (SEQ. ID NO: 141)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 132) (SEQ. ID NO: 142)
10 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 133) (SEQ. ID NO: 143)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 134) (SEQ. ID NO: 144)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 135) (SEQ. ID NO: 145)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 136) (SEQ. ID NO: 146)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 137) (SEQ. ID NO: 147)
15 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 138) (SEQ. ID NO: 148)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 139) (SEQ. ID NO: 149)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 140) (SEQ. ID NO: 150)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 141) (SEQ. ID NO: 151)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 142) (SEQ. ID NO: 152)
20 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 143) (SEQ. ID NO: 153)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 144) (SEQ. ID NO: 154)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 145) (SEQ. ID NO: 155)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 146) (SEQ. ID NO: 156)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 147) (SEQ. ID NO: 157)
25 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 148) (SEQ. ID NO: 158)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 149) (SEQ. ID NO: 159)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 150) (SEQ. ID NO: 160)
5'-C GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 151) (SEQ. ID NO: 161)
5'-C GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 152) (SEQ. ID NO: 162)
30 5'-C GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 153) (SEQ. ID NO: 163)
5'-C GGC CTG GAA AGC TGA GAT GG -3' (FRAG 154) (SEQ. ID NO: 164)
5'-C GGC CTG GAA AGC TGA GAT G -3' (FRAG 155) (SEQ. ID NO: 165)
5'-C GGC CTG GAA AGC TGA GAT -3' (FRAG 156) (SEQ. ID NO: 166)
5'-C GGC CTG GAA AGC TGA GA-3' (FRAG 157) (SEQ. ID NO: 167)
35 5'-C GGC CTG GAA AGC TGA G-3' (FRAG 158) (SEQ. ID NO: 168)
5'-C GGC CTG GAA AGC TGA-3' (FRAG 159) (SEQ. ID NO: 169)
5'-C GGC CTG GAA AGC TG-3' (FRAG 160) (SEQ. ID NO: 170)
5'-C GGC CTG GAA AGC T-3' (FRAG 161) (SEQ. ID NO: 171)
5'-C GGC CTG GAA AGC-3' (FRAG 162) (SEQ. ID NO: 172)
40 5'-C GGC CTG GAA AG-3' (FRAG 163) (SEQ. ID NO: 173)
5'-C GGC CTG GAA A-3' (FRAG 164) (SEQ. ID NO: 174)
5'-C GGC CTG GAA-3' (FRAG 165) (SEQ. ID NO: 175)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 166) (SEQ. ID NO: 176)
45 5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 167) (SEQ. ID NO: 177)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 168) (SEQ. ID NO: 178)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 169) (SEQ. ID NO: 179)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 170) (SEQ. ID NO: 180)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 171) (SEQ. ID NO: 181)
50 5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 172) (SEQ. ID NO: 182)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 173) (SEQ. ID NO: 183)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 174) (SEQ. ID NO: 184)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 175) (SEQ. ID NO: 185)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 176) (SEQ. ID NO: 186)
55 5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 177) (SEQ. ID NO: 187)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 178) (SEQ. ID NO: 188)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 179) (SEQ. ID NO: 189)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 180) (SEQ. ID NO: 190)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 181) (SEQ. ID NO: 191)
60 5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 182) (SEQ. ID NO: 192)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 183) (SEQ. ID NO: 193)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 184) (SEQ. ID NO: 194)

- 5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 185) (SEQ. ID NO: 195)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 186) (SEQ. ID NO: 196)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 187) (SEQ. ID NO: 197)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 188) (SEQ. ID NO: 198)
5 5'- GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 189) (SEQ. ID NO: 199)
5'- GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 190) (SEQ. ID NO: 200)
5'- GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 191) (SEQ. ID NO: 201)
5'- GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 192) (SEQ. ID NO: 202)
5'- GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 193) (SEQ. ID NO: 203)
10 5'- GGC CTG GAA AGC TGA GAT GG -3' (FRAG 194) (SEQ. ID NO: 204)
5'- GGC CTG GAA AGC TGA GAT G -3' (FRAG 195) (SEQ. ID NO: 205)
5'- GGC CTG GAA AGC TGA GAT -3' (FRAG 196) (SEQ. ID NO: 206)
5'- GGC CTG GAA AGC TGA GA-3' (FRAG 197) (SEQ. ID NO: 207)
5'- GGC CTG GAA AGC TGA G-3' (FRAG 198) (SEQ. ID NO: 208)
15 5'- GGC CTG GAA AGC TGA-3' (FRAG 199) (SEQ. ID NO: 209)
5'- GGC CTG GAA AGC TG-3' (FRAG 200) (SEQ. ID NO: 210)
5'- GGC CTG GAA AGC T-3' (FRAG 201) (SEQ. ID NO: 211)
5'- GGC CTG GAA AGC-3' (FRAG 202) (SEQ. ID NO: 212)
5'- GGC CTG GAA AG-3' (FRAG 203) (SEQ. ID NO: 213)
20 5'- GGC CTG GAA A-3' (FRAG 204) (SEQ. ID NO: 214)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 205) (SEQ. ID NO: 215)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 206) (SEQ. ID NO: 216)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 207) (SEQ. ID NO: 217)
25 5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 208) (SEQ. ID NO: 218)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 209) (SEQ. ID NO: 219)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 210) (SEQ. ID NO: 220)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 211) (SEQ. ID NO: 221)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 212) (SEQ. ID NO: 222)
30 5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 213) (SEQ. ID NO: 223)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 214) (SEQ. ID NO: 224)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 215) (SEQ. ID NO: 225)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 216) (SEQ. ID NO: 226)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 217) (SEQ. ID NO: 227)
35 5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 218) (SEQ. ID NO: 228)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 219) (SEQ. ID NO: 229)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 220) (SEQ. ID NO: 230)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 221) (SEQ. ID NO: 231)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 222) (SEQ. ID NO: 232)
40 5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 223) (SEQ. ID NO: 233)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 224) (SEQ. ID NO: 234)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 225) (SEQ. ID NO: 235)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 226) (SEQ. ID NO: 236)
5'- GC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 227) (SEQ. ID NO: 237)
45 5'- GC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 228) (SEQ. ID NO: 238)
5'- GC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 229) (SEQ. ID NO: 239)
5'- GC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 230) (SEQ. ID NO: 240)
5'- GC CTG GAA AGC TGA GAT GGA G -3' (FRAG 231) (SEQ. ID NO: 241)
5'- GC CTG GAA AGC TGA GAT GGA -3' (FRAG 232) (SEQ. ID NO: 242)
50 5'- GC CTG GAA AGC TGA GAT GG -3' (FRAG 233) (SEQ. ID NO: 243)
5'- GC CTG GAA AGC TGA GAT G -3' (FRAG 234) (SEQ. ID NO: 244)
5'- GC CTG GAA AGC TGA GAT -3' (FRAG 235) (SEQ. ID NO: 245)
5'- GC CTG GAA AGC TGA GA-3' (FRAG 236) (SEQ. ID NO: 246)
5'- GC CTG GAA AGC TGA G-3' (FRAG 237) (SEQ. ID NO: 247)
55 5'- GC CTG GAA AGC TGA-3' (FRAG 238) (SEQ. ID NO: 248)
5'- GC CTG GAA AGC TG-3' (FRAG 239) (SEQ. ID NO: 249)
5'- GC CTG GAA AGC T-3' (FRAG 240) (SEQ. ID NO: 250)
5'- GC CTG GAA AGC-3' (FRAG 241) (SEQ. ID NO: 251)
5'- GC CTG GAA AG-3' (FRAG 242) (SEQ. ID NO: 252)
60 5'- C CTG GAA AGC TGA GAT GG A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 243) (SEQ. ID NO: 253)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 244) (SEQ. ID NO: 254)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 245) (SEQ. ID NO: 255)

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- 5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 246) (SEQ. ID NO: 256)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 247) (SEQ. ID NO: 257)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 248) (SEQ. ID NO: 258)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 249) (SEQ. ID NO: 259)
5 5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 250) (SEQ. ID NO: 260)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 251) (SEQ. ID NO: 261)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 252) (SEQ. ID NO: 262)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 253) (SEQ. ID NO: 263)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 254) (SEQ. ID NO: 264)
10 5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 255) (SEQ. ID NO: 265)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 256) (SEQ. ID NO: 266)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 257) (SEQ. ID NO: 267)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 258) (SEQ. ID NO: 268)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 259) (SEQ. ID NO: 269)
15 5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 260) (SEQ. ID NO: 270)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 261) (SEQ. ID NO: 271)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 262) (SEQ. ID NO: 272)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 263) (SEQ. ID NO: 273)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 264) (SEQ. ID NO: 274)
20 5'- C CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 265) (SEQ. ID NO: 275)
5'- C CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 266) (SEQ. ID NO: 276)
5'- C CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 267) (SEQ. ID NO: 277)
5'- C CTG GAA AGC TGA GAT GGA GG -3' (FRAG 268) (SEQ. ID NO: 278)
5'- C CTG GAA AGC TGA GAT GGA G -3' (FRAG 269) (SEQ. ID NO: 279)
25 5'- C CTG GAA AGC TGA GAT GGA -3' (FRAG 270) (SEQ. ID NO: 280)
5'- C CTG GAA AGC TGA GAT GG -3' (FRAG 271) (SEQ. ID NO: 281)
5'- C CTG GAA AGC TGA GAT G -3' (FRAG 272) (SEQ. ID NO: 282)
5'- C CTG GAA AGC TGA GAT -3' (FRAG 273) (SEQ. ID NO: 283)
5'- C CTG GAA AGC TGA GA-3' (FRAG 274) (SEQ. ID NO: 284)
30 5'- C CTG GAA AGC TGA G-3' (FRAG 275) (SEQ. ID NO: 285)
5'- C CTG GAA AGC TGA-3' (FRAG 276) (SEQ. ID NO: 286)
5'- C CTG GAA AGC TG-3' (FRAG 277) (SEQ. ID NO: 287)
5'- C CTG GAA AGC T-3' (FRAG 278) (SEQ. ID NO: 288)
5'- C CTG GAA AGC-3' (FRAG 279) (SEQ. ID NO: 289)
35 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 280) (SEQ. ID NO: 290)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 281) (SEQ. ID NO: 291)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 282) (SEQ. ID NO: 292)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 283) (SEQ. ID NO: 293)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 284) (SEQ. ID NO: 294)
40 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 285) (SEQ. ID NO: 295)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 286) (SEQ. ID NO: 296)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 287) (SEQ. ID NO: 297)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 288) (SEQ. ID NO: 298)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 289) (SEQ. ID NO: 299)
45 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 290) (SEQ. ID NO: 300)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 291) (SEQ. ID NO: 301)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 292) (SEQ. ID NO: 302)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 293) (SEQ. ID NO: 303)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 294) (SEQ. ID NO: 304)
50 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 295) (SEQ. ID NO: 305)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 296) (SEQ. ID NO: 306)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 297) (SEQ. ID NO: 307)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 298) (SEQ. ID NO: 308)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 299) (SEQ. ID NO: 309)
55 5'- CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 300) (SEQ. ID NO: 310)
5'- CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 301) (SEQ. ID NO: 311)
5'- CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 302) (SEQ. ID NO: 312)
5'- CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 303) (SEQ. ID NO: 313)
5'- CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 304) (SEQ. ID NO: 314)
60 5'- CTG GAA AGC TGA GAT GGA GG -3' (FRAG 305) (SEQ. ID NO: 315)
5'- CTG GAA AGC TGA GAT GGA G -3' (FRAG 306) (SEQ. ID NO: 316)
5'- CTG GAA AGC TGA GAT GGA -3' (FRAG 307) (SEQ. ID NO: 317)

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- 5'- CTG GAA AGC TGA GAT GG -3' (FRAG 308) (SEQ. ID NO: 318)
5'- CTG GAA AGC TGA GAT G -3' (FRAG 309) (SEQ. ID NO: 319)
5'- CTG GAA AGC TGA GAT -3' (FRAG 310) (SEQ. ID NO: 320)
5'- CTG GAA AGC TGA GA-3' (FRAG 311) (SEQ. ID NO: 321)
5 5'- CTG GAA AGC TGA G-3' (FRAG 312) (SEQ. ID NO: 322)
5'- CTG GAA AGC TGA-3' (FRAG 313) (SEQ. ID NO: 323)
5'- CTG GAA AGC TG-3' (FRAG 314) (SEQ. ID NO: 324)
5'- CTG GAA AGC T-3' (FRAG 315) (SEQ. ID NO: 325)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 316) (SEQ. ID NO: 326)
10 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 317) (SEQ. ID NO: 327)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 318) (SEQ. ID NO: 328)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 319) (SEQ. ID NO: 329)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 320) (SEQ. ID NO: 330)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 321) (SEQ. ID NO: 331)
15 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 322) (SEQ. ID NO: 332)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 323) (SEQ. ID NO: 333)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 324) (SEQ. ID NO: 334)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 325) (SEQ. ID NO: 335)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 326) (SEQ. ID NO: 336)
20 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 327) (SEQ. ID NO: 337)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 328) (SEQ. ID NO: 338)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 329) (SEQ. ID NO: 339)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 330) (SEQ. ID NO: 340)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 331) (SEQ. ID NO: 341)
25 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 332) (SEQ. ID NO: 342)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 333) (SEQ. ID NO: 343)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 334) (SEQ. ID NO: 344)
5'- TG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 335) (SEQ. ID NO: 345)
5'- TG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 336) (SEQ. ID NO: 346)
30 5'- TG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 337) (SEQ. ID NO: 347)
5'- TG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 338) (SEQ. ID NO: 348)
5'- TG GAA AGC TGA GAT GGA GGG C -3' (FRAG 339) (SEQ. ID NO: 349)
5'- TG GAA AGC TGA GAT GGA GGG -3' (FRAG 340) (SEQ. ID NO: 350)
5'- TG GAA AGC TGA GAT GGA GG -3' (FRAG 341) (SEQ. ID NO: 351)
35 5'- TG GAA AGC TGA GAT GGA G -3' (FRAG 342) (SEQ. ID NO: 352)
5'- TG GAA AGC TGA GAT GGA -3' (FRAG 343) (SEQ. ID NO: 353)
5'- TG GAA AGC TGA GAT GG -3' (FRAG 344) (SEQ. ID NO: 354)
5'- TG GAA AGC TGA GAT G -3' (FRAG 345) (SEQ. ID NO: 355)
5'- TG GAA AGC TGA GAT -3' (FRAG 346) (SEQ. ID NO: 356)
40 5'- TG GAA AGC TGA GA-3' (FRAG 347) (SEQ. ID NO: 357)
5'- TG GAA AGC TGA G-3' (FRAG 348) (SEQ. ID NO: 358)
5'- TG GAA AGC TGA-3' (FRAG 349) (SEQ. ID NO: 359)
5'- TG GAA AGC TG-3' (FRAG 350) (SEQ. ID NO: 360)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 351) (SEQ. ID NO: 361)
45 5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 352) (SEQ. ID NO: 362)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 353) (SEQ. ID NO: 363)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 354) (SEQ. ID NO: 364)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 355) (SEQ. ID NO: 365)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 356) (SEQ. ID NO: 366)
50 5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 357) (SEQ. ID NO: 367)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 358) (SEQ. ID NO: 368)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 359) (SEQ. ID NO: 369)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 360) (SEQ. ID NO: 370)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 361) (SEQ. ID NO: 371)
55 5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 362) (SEQ. ID NO: 372)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 363) (SEQ. ID NO: 373)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 364) (SEQ. ID NO: 374)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 365) (SEQ. ID NO: 375)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 366) (SEQ. ID NO: 376)
60 5'- G GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 367) (SEQ. ID NO: 377)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 368) (SEQ. ID NO: 378)
5'- G GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 369) (SEQ. ID NO: 379)

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- 5'- G GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 370) (SEQ. ID NO: 380)
5'- G GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 371) (SEQ. ID NO: 381)
5'- G GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 372) (SEQ. ID NO: 382)
5'- G GAA AGC TGA GAT GGA GGG CG -3' (FRAG 373) (SEQ. ID NO: 383)
5 5'- G GAA AGC TGA GAT GGA GGG C -3' (FRAG 374) (SEQ. ID NO: 384)
5'- G GAA AGC TGA GAT GGA GGG -3' (FRAG 375) (SEQ. ID NO: 385)
5'- G GAA AGC TGA GAT GGA GG -3' (FRAG 376) (SEQ. ID NO: 386)
5'- G GAA AGC TGA GAT GGA G -3' (FRAG 377) (SEQ. ID NO: 387)
5'- G GAA AGC TGA GAT GGA -3' (FRAG 378) (SEQ. ID NO: 388)
10 5'- G GAA AGC TGA GAT GG -3' (FRAG 379) (SEQ. ID NO: 389)
5'- G GAA AGC TGA GAT G -3' (FRAG 380) (SEQ. ID NO: 390)
5'- G GAA AGC TGA GAT -3' (FRAG 381) (SEQ. ID NO: 391)
5'- G GAA AGC TGA GA-3' (FRAG 382) (SEQ. ID NO: 392)
5'- G GAA AGC TGA G-3' (FRAG 383) (SEQ. ID NO: 393)
15 5'- G GAA AGC TGA-3' (FRAG 384) (SEQ. ID NO: 394)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 385) (SEQ. ID NO: 395)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 386) (SEQ. ID NO: 396)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 387) (SEQ. ID NO: 397)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 388) (SEQ. ID NO: 398)
20 5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 389) (SEQ. ID NO: 399)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 390) (SEQ. ID NO: 400)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 391) (SEQ. ID NO: 401)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 392) (SEQ. ID NO: 402)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 393) (SEQ. ID NO: 403)
25 5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 394) (SEQ. ID NO: 404)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 395) (SEQ. ID NO: 405)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 396) (SEQ. ID NO: 406)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 397) (SEQ. ID NO: 407)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 398) (SEQ. ID NO: 408)
30 5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 399) (SEQ. ID NO: 409)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 400) (SEQ. ID NO: 410)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 401) (SEQ. ID NO: 411)
5'- GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 402) (SEQ. ID NO: 412)
5'- GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 403) (SEQ. ID NO: 413)
35 5'- GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 404) (SEQ. ID NO: 414)
5'- GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 405) (SEQ. ID NO: 415)
5'- GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 406) (SEQ. ID NO: 416)
5'- GAA AGC TGA GAT GGA GGG CG -3' (FRAG 407) (SEQ. ID NO: 417)
5'- GAA AGC TGA GAT GGA GGG C -3' (FRAG 408) (SEQ. ID NO: 418)
40 5'- GAA AGC TGA GAT GGA GGG -3' (FRAG 409) (SEQ. ID NO: 419)
5'- GAA AGC TGA GAT GGA GG -3' (FRAG 410) (SEQ. ID NO: 420)
5'- GAA AGC TGA GAT GGA G -3' (FRAG 411) (SEQ. ID NO: 421)
5'- GAA AGC TGA GAT GGA -3' (FRAG 412) (SEQ. ID NO: 422)
5'- GAA AGC TGA GAT GG -3' (FRAG 413) (SEQ. ID NO: 423)
45 5'- GAA AGC TGA GAT G -3' (FRAG 414) (SEQ. ID NO: 424)
5'- GAA AGC TGA GAT -3' (FRAG 415) (SEQ. ID NO: 425)
5'- GAA AGC TGA GA-3' (FRAG 416) (SEQ. ID NO: 426)
5'- GAA AGC TGA G-3' (FRAG 417) (SEQ. ID NO: 427)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 418) (SEQ. ID NO: 428)
50 5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 419) (SEQ. ID NO: 429)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 420) (SEQ. ID NO: 430)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 421) (SEQ. ID NO: 431)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 422) (SEQ. ID NO: 432)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 423) (SEQ. ID NO: 433)
55 5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 424) (SEQ. ID NO: 434)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 425) (SEQ. ID NO: 435)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 426) (SEQ. ID NO: 436)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 427) (SEQ. ID NO: 437)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 428) (SEQ. ID NO: 438)
60 5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 429) (SEQ. ID NO: 439)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 430) (SEQ. ID NO: 440)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 431) (SEQ. ID NO: 441)

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- 5'- AA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 432) (SEQ. ID NO: 442)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 433) (SEQ. ID NO: 443)
5'- AA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 434) (SEQ. ID NO: 444)
5'- AA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 435) (SEQ. ID NO: 445)
5 5'- AA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 436) (SEQ. ID NO: 446)
5'- AA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 437) (SEQ. ID NO: 447)
5'- AA AGC TGA GAT GGA GGG CGG C-3' (FRAG 438) (SEQ. ID NO: 448)
5'- AA AGC TGA GAT GGA GGG CGG -3' (FRAG 439) (SEQ. ID NO: 449)
5'- AA AGC TGA GAT GGA GGG CG -3' (FRAG 440) (SEQ. ID NO: 450)
10 5'- AA AGC TGA GAT GGA GGG C -3' (FRAG 441) (SEQ. ID NO: 451)
5'- AA AGC TGA GAT GGA GGG -3' (FRAG 442) (SEQ. ID NO: 452)
5'- AA AGC TGA GAT GGA GG -3' (FRAG 443) (SEQ. ID NO: 453)
5'- AA AGC TGA GAT GGA G -3' (FRAG 444) (SEQ. ID NO: 454)
5'- AA AGC TGA GAT GGA -3' (FRAG 445) (SEQ. ID NO: 455)
15 5'- AA AGC TGA GAT GG -3' (FRAG 446) (SEQ. ID NO: 456)
5'- AA AGC TGA GAT G -3' (FRAG 447) (SEQ. ID NO: 457)
5'- AA AGC TGA GAT -3' (FRAG 448) (SEQ. ID NO: 458)
5'- AA AGC TGA GA-3' (FRAG 449) (SEQ. ID NO: 459)
5'- A AGC TGA GAT GGA GGG CG G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 450) (SEQ. ID NO: 460)
20 5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 451) (SEQ. ID NO: 461)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 452) (SEQ. ID NO: 462)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 453) (SEQ. ID NO: 463)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 454) (SEQ. ID NO: 464)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 455) (SEQ. ID NO: 465)
25 5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 456) (SEQ. ID NO: 466)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 457) (SEQ. ID NO: 467)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 458) (SEQ. ID NO: 468)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 459) (SEQ. ID NO: 469)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 460) (SEQ. ID NO: 470)
30 5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 461) (SEQ. ID NO: 471)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 462) (SEQ. ID NO: 472)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 463) (SEQ. ID NO: 473)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 464) (SEQ. ID NO: 474)
5'- A AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 465) (SEQ. ID NO: 475)
35 5'- A AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 466) (SEQ. ID NO: 476)
5'- A AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 467) (SEQ. ID NO: 477)
5'- A AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 468) (SEQ. ID NO: 478)
5'- A AGC TGA GAT GGA GGG CGG CA-3' (FRAG 469) (SEQ. ID NO: 479)
5'- A AGC TGA GAT GGA GGG CGG C-3' (FRAG 470) (SEQ. ID NO: 480)
40 5'- A AGC TGA GAT GGA GGG CGG -3' (FRAG 471) (SEQ. ID NO: 481)
5'- A AGC TGA GAT GGA GGG CG -3' (FRAG 472) (SEQ. ID NO: 482)
5'- A AGC TGA GAT GGA GGG C -3' (FRAG 473) (SEQ. ID NO: 483)
5'- A AGC TGA GAT GGA GGG -3' (FRAG 474) (SEQ. ID NO: 484)
5'- A AGC TGA GAT GGA GG -3' (FRAG 475) (SEQ. ID NO: 485)
45 5'- A AGC TGA GAT GGA G -3' (FRAG 476) (SEQ. ID NO: 486)
5'- A AGC TGA GAT GGA -3' (FRAG 477) (SEQ. ID NO: 487)
5'- A AGC TGA GAT GG -3' (FRAG 478) (SEQ. ID NO: 488)
5'- A AGC TGA GAT G -3' (FRAG 479) (SEQ. ID NO: 489)
5'- A AGC TGA GAT -3' (FRAG 480) (SEQ. ID NO: 490)
50 5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 481) (SEQ. ID NO: 491)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 482) (SEQ. ID NO: 492)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 483) (SEQ. ID NO: 493)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 484) (SEQ. ID NO: 494)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 485) (SEQ. ID NO: 495)
55 5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 486) (SEQ. ID NO: 496)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 487) (SEQ. ID NO: 497)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 488) (SEQ. ID NO: 498)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 489) (SEQ. ID NO: 499)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 490) (SEQ. ID NO: 500)
60 5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 491) (SEQ. ID NO: 501)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 492) (SEQ. ID NO: 502)
5'- AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 493) (SEQ. ID NO: 503)

- 5'- AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 494) (SEQ. ID NO: 504)
5'- AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 495) (SEQ. ID NO: 505)
5'- AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 496) (SEQ. ID NO: 506)
5'- AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 497) (SEQ. ID NO: 507)
5 5'- AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 498) (SEQ. ID NO: 508)
5'- AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 499) (SEQ. ID NO: 509)
5'- AGC TGA GAT GGA GGG CGG CA-3' (FRAG 500) (SEQ. ID NO: 510)
5'- AGC TGA GAT GGA GGG CGG C-3' (FRAG 501) (SEQ. ID NO: 511)
5'- AGC TGA GAT GGA GGG CGG -3' (FRAG 502) (SEQ. ID NO: 512)
10 5'- AGC TGA GAT GGA GGG CG -3' (FRAG 503) (SEQ. ID NO: 513)
5'- AGC TGA GAT GGA GGG C -3' (FRAG 504) (SEQ. ID NO: 514)
5'- AGC TGA GAT GGA GGG -3' (FRAG 505) (SEQ. ID NO: 515)
5'- AGC TGA GAT GGA GG -3' (FRAG 506) (SEQ. ID NO: 516)
5'- AGC TGA GAT GGA G -3' (FRAG 507) (SEQ. ID NO: 517)
15 5'- AGC TGA GAT GGA -3' (FRAG 508) (SEQ. ID NO: 518)
5'- AGC TGA GAT GG -3' (FRAG 509) (SEQ. ID NO: 519)
5'- AGC TGA GAT G -3' (FRAG 510) (SEQ. ID NO: 520)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 511) (SEQ. ID NO: 521)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 512) (SEQ. ID NO: 522)
20 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 513) (SEQ. ID NO: 523)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 514) (SEQ. ID NO: 524)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 515) (SEQ. ID NO: 525)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 516) (SEQ. ID NO: 526)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 517) (SEQ. ID NO: 527)
25 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 518) (SEQ. ID NO: 528)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 519) (SEQ. ID NO: 529)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 520) (SEQ. ID NO: 530)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 521) (SEQ. ID NO: 531)
5'- GC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 522) (SEQ. ID NO: 532)
30 5'- GC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 523) (SEQ. ID NO: 533)
5'- GC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 524) (SEQ. ID NO: 534)
5'- GC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 525) (SEQ. ID NO: 535)
5'- GC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 526) (SEQ. ID NO: 536)
5'- GC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 527) (SEQ. ID NO: 537)
35 5'- GC TGA GAT GGA GGG CGG CAT G -3' (FRAG 528) (SEQ. ID NO: 538)
5'- GC TGA GAT GGA GGG CGG CAT -3' (FRAG 529) (SEQ. ID NO: 539)
5'- GC TGA GAT GGA GGG CGG CA-3' (FRAG 530) (SEQ. ID NO: 540)
5'- GC TGA GAT GGA GGG CGG C-3' (FRAG 531) (SEQ. ID NO: 541)
5'- GC TGA GAT GGA GGG CGG -3' (FRAG 532) (SEQ. ID NO: 542)
40 5'- GC TGA GAT GGA GGG CG -3' (FRAG 533) (SEQ. ID NO: 543)
5'- GC TGA GAT GGA GGG C -3' (FRAG 534) (SEQ. ID NO: 544)
5'- GC TGA GAT GGA GGG -3' (FRAG 535) (SEQ. ID NO: 545)
5'- GC TGA GAT GGA GG -3' (FRAG 536) (SEQ. ID NO: 546)
5'- GC TGA GAT GGA G -3' (FRAG 537) (SEQ. ID NO: 547)
45 5'- GC TGA GAT GGA -3' (FRAG 538) (SEQ. ID NO: 548)
5'- GC TGA GAT GG -3' (FRAG 539) (SEQ. ID NO: 549)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 540) (SEQ. ID NO: 550)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 541) (SEQ. ID NO: 551)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 542) (SEQ. ID NO: 552)
50 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 543) (SEQ. ID NO: 553)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 544) (SEQ. ID NO: 554)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 545) (SEQ. ID NO: 555)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 546) (SEQ. ID NO: 556)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 547) (SEQ. ID NO: 557)
55 5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 548) (SEQ. ID NO: 558)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 549) (SEQ. ID NO: 559)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 550) (SEQ. ID NO: 560)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 551) (SEQ. ID NO: 561)
5'- C TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 552) (SEQ. ID NO: 562)
60 5'- C TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 553) (SEQ. ID NO: 563)
5'- C TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 554) (SEQ. ID NO: 564)
5'- C TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 555) (SEQ. ID NO: 565)

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5'- C TGA GAT GGA GGG CGG CAT GG -3' (FRAG 556) (SEQ. ID NO: 566)
5'- C TGA GAT GGA GGG CGG CAT G -3' (FRAG 557) (SEQ. ID NO: 567)
5'- C TGA GAT GGA GGG CGG CAT -3' (FRAG 558) (SEQ. ID NO: 568)
5'- C TGA GAT GGA GGG CGG CA-3' (FRAG 559) (SEQ. ID NO: 569)
5 5'- C TGA GAT GGA GGG CGG C-3' (FRAG 560) (SEQ. ID NO: 570)
5'- C TGA GAT GGA GGG CGG -3' (FRAG 561) (SEQ. ID NO: 571)
5'- C TGA GAT GGA GGG CG -3' (FRAG 562) (SEQ. ID NO: 572)
5'- C TGA GAT GGA GGG C -3' (FRAG 563) (SEQ. ID NO: 573)
5'- C TGA GAT GGA GGG -3' (FRAG 564) (SEQ. ID NO: 574)
10 5'- C TGA GAT GGA GG -3' (FRAG 565) (SEQ. ID NO: 575)
5'- C TGA GAT GGA G -3' (FRAG 566) (SEQ. ID NO: 576)
5'- C TGA GAT GGA -3' (FRAG 567) (SEQ. ID NO: 577)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 568) (SEQ. ID NO: 578)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 569) (SEQ. ID NO: 579)
15 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 570) (SEQ. ID NO: 580)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 571) (SEQ. ID NO: 581)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 572) (SEQ. ID NO: 582)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 573) (SEQ. ID NO: 583)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 574) (SEQ. ID NO: 584)
20 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 575) (SEQ. ID NO: 585)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 576) (SEQ. ID NO: 586)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 577) (SEQ. ID NO: 587)
5'- TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 578) (SEQ. ID NO: 588)
5'- TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 579) (SEQ. ID NO: 589)
25 5'- TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 580) (SEQ. ID NO: 590)
5'- TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 581) (SEQ. ID NO: 591)
5'- TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 582) (SEQ. ID NO: 592)
5'- TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 583) (SEQ. ID NO: 593)
5'- TGA GAT GGA GGG CGG CAT GG -3' (FRAG 584) (SEQ. ID NO: 594)
30 5'- TGA GAT GGA GGG CGG CAT G -3' (FRAG 585) (SEQ. ID NO: 595)
5'- TGA GAT GGA GGG CGG CAT -3' (FRAG 586) (SEQ. ID NO: 596)
5'- TGA GAT GGA GGG CGG CA-3' (FRAG 587) (SEQ. ID NO: 597)
5'- TGA GAT GGA GGG CGG C-3' (FRAG 588) (SEQ. ID NO: 598)
5'- TGA GAT GGA GGG CGG -3' (FRAG 589) (SEQ. ID NO: 599)
35 5'- TGA GAT GGA GGG CG -3' (FRAG 590) (SEQ. ID NO: 600)
5'- TGA GAT GGA GGG C -3' (FRAG 591) (SEQ. ID NO: 601)
5'- TGA GAT GGA GGG -3' (FRAG 592) (SEQ. ID NO: 602)
5'- TGA GAT GGA GG -3' (FRAG 593) (SEQ. ID NO: 603)
5'- TGA GAT GGA G -3' (FRAG 594) (SEQ. ID NO: 604)
40 5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 595) (SEQ. ID NO: 605)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 596) (SEQ. ID NO: 606)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 597) (SEQ. ID NO: 607)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 598) (SEQ. ID NO: 608)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 599) (SEQ. ID NO: 609)
45 5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 600) (SEQ. ID NO: 610)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 601) (SEQ. ID NO: 611)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 602) (SEQ. ID NO: 612)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 603) (SEQ. ID NO: 613)
5'- GA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 604) (SEQ. ID NO: 614)
50 5'- GA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 605) (SEQ. ID NO: 615)
5'- GA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 606) (SEQ. ID NO: 616)
5'- GA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 607) (SEQ. ID NO: 617)
5'- GA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 608) (SEQ. ID NO: 618)
5'- GA GAT GGA GGG CGG CAT GGC G-3' (FRAG 609) (SEQ. ID NO: 619)
55 5'- GA GAT GGA GGG CGG CAT GGC -3' (FRAG 610) (SEQ. ID NO: 620)
5'- GA GAT GGA GGG CGG CAT GG -3' (FRAG 611) (SEQ. ID NO: 621)
5'- GA GAT GGA GGG CGG CAT G -3' (FRAG 612) (SEQ. ID NO: 622)
5'- GA GAT GGA GGG CGG CAT -3' (FRAG 613) (SEQ. ID NO: 623)
5'- GA GAT GGA GGG CGG CA-3' (FRAG 614) (SEQ. ID NO: 624)
60 5'- GA GAT GGA GGG CGG C-3' (FRAG 615) (SEQ. ID NO: 625)
5'- GA GAT GGA GGG CGG -3' (FRAG 616) (SEQ. ID NO: 626)
5'- GA GAT GGA GGG CG -3' (FRAG 617) (SEQ. ID NO: 627)

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- 5'- GA GAT GGA GGG C -3' (FRAG 618) (SEQ. ID NO: 628)
5'- GA GAT GGA GGG -3' (FRAG 619) (SEQ. ID NO: 629)
5'- GA GAT GGA GG -3' (FRAG 620) (SEQ. ID NO: 630)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 621) (SEQ. ID NO: 631)
5 A 5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 622) (SEQ. ID NO: 632)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 623) (SEQ. ID NO: 633)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 624) (SEQ. ID NO: 634)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 625) (SEQ. ID NO: 635)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 626) (SEQ. ID NO: 636)
10 5'- A GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 627) (SEQ. ID NO: 637)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 628) (SEQ. ID NO: 638)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 629) (SEQ. ID NO: 639)
5'- A GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 630) (SEQ. ID NO: 640)
5'- A GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 631) (SEQ. ID NO: 641)
15 5'- A GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 632) (SEQ. ID NO: 642)
5'- A GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 633) (SEQ. ID NO: 643)
5'- A GAT GGA GGG CGG CAT GGC GG-3' (FRAG 634) (SEQ. ID NO: 644)
5'- A GAT GGA GGG CGG CAT GGC G-3' (FRAG 635) (SEQ. ID NO: 645)
5'- A GAT GGA GGG CGG CAT GGC -3' (FRAG 636) (SEQ. ID NO: 646)
20 5'- A GAT GGA GGG CGG CAT GG -3' (FRAG 637) (SEQ. ID NO: 647)
5'- A GAT GGA GGG CGG CAT G -3' (FRAG 638) (SEQ. ID NO: 648)
5'- A GAT GGA GGG CGG CAT -3' (FRAG 639) (SEQ. ID NO: 649)
5'- A GAT GGA GGG CGG CA-3' (FRAG 640) (SEQ. ID NO: 650)
5'- A GAT GGA GGG CGG C-3' (FRAG 641) (SEQ. ID NO: 651)
25 5'- A GAT GGA GGG CGG -3' (FRAG 642) (SEQ. ID NO: 652)
5'- A GAT GGA GGG CG -3' (FRAG 643) (SEQ. ID NO: 653)
5'- A GAT GGA GGG C -3' (FRAG 644) (SEQ. ID NO: 654)
5'- A GAT GGA GGG -3' (FRAG 645) (SEQ. ID NO: 655)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 646) (SEQ. ID NO: 656)
30 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 647) (SEQ. ID NO: 657)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 648) (SEQ. ID NO: 658)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 649) (SEQ. ID NO: 659)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 650) (SEQ. ID NO: 660)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 651) (SEQ. ID NO: 661)
35 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 652) (SEQ. ID NO: 662)
5'- GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 653) (SEQ. ID NO: 663)
5'- GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 654) (SEQ. ID NO: 664)
5'- GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 655) (SEQ. ID NO: 665)
5'- GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 656) (SEQ. ID NO: 666)
40 5'- GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 657) (SEQ. ID NO: 667)
5'- GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 658) (SEQ. ID NO: 668)
5'- GAT GGA GGG CGG CAT GGC GG-3' (FRAG 659) (SEQ. ID NO: 669)
5'- GAT GGA GGG CGG CAT GGC G-3' (FRAG 660) (SEQ. ID NO: 670)
5'- GAT GGA GGG CGG CAT GGC -3' (FRAG 661) (SEQ. ID NO: 671)
45 5'- GAT GGA GGG CGG CAT GG -3' (FRAG 662) (SEQ. ID NO: 672)
5'- GAT GGA GGG CGG CAT G -3' (FRAG 663) (SEQ. ID NO: 673)
5'- GAT GGA GGG CGG CAT -3' (FRAG 664) (SEQ. ID NO: 674)
5'- GAT GGA GGG CGG CA-3' (FRAG 665) (SEQ. ID NO: 675)
5'- GAT GGA GGG CGG C-3' (FRAG 666) (SEQ. ID NO: 676)
50 5'- GAT GGA GGG CGG -3' (FRAG 667) (SEQ. ID NO: 677)
5'- GAT GGA GGG CG -3' (FRAG 668) (SEQ. ID NO: 678)
5'- GAT GGA GGG C -3' (FRAG 669) (SEQ. ID NO: 679)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 670) (SEQ. ID NO: 680)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 671) (SEQ. ID NO: 681)
55 5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 672) (SEQ. ID NO: 682)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 673) (SEQ. ID NO: 683)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 674) (SEQ. ID NO: 684)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 675) (SEQ. ID NO: 685)
5'- AT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 676) (SEQ. ID NO: 686)
60 5'- AT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 677) (SEQ. ID NO: 687)
5'- AT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 678) (SEQ. ID NO: 688)
5'- AT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 679) (SEQ. ID NO: 689)

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- 5'- AT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 680) (SEQ. ID NO: 690)
5'- AT GGA GGG CGG CAT GGC GGG C-3' (FRAG 681) (SEQ. ID NO: 691)
5'- AT GGA GGG CGG CAT GGC GGG -3' (FRAG 682) (SEQ. ID NO: 692)
5'- AT GGA GGG CGG CAT GGC GG-3' (FRAG 683) (SEQ. ID NO: 693)
5 5'- AT GGA GGG CGG CAT GGC G-3' (FRAG 684) (SEQ. ID NO: 694)
5'- AT GGA GGG CGG CAT GGC -3' (FRAG 685) (SEQ. ID NO: 695)
5'- AT GGA GGG CGG CAT GG -3' (FRAG 686) (SEQ. ID NO: 696)
5'- AT GGA GGG CGG CAT G -3' (FRAG 687) (SEQ. ID NO: 697)
5'- AT GGA GGG CGG CAT -3' (FRAG 688) (SEQ. ID NO: 698)
10 5'- AT GGA GGG CGG CA-3' (FRAG 689) (SEQ. ID NO: 699)
5'- AT GGA GGG CGG C-3' (FRAG 690) (SEQ. ID NO: 700)
5'- AT GGA GGG CGG -3' (FRAG 691) (SEQ. ID NO: 701)
5'- AT GGA GGG CG -3' (FRAG 692) (SEQ. ID NO: 702)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 693) (SEQ. ID NO: 703)
15 5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 694) (SEQ. ID NO: 704)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 695) (SEQ. ID NO: 705)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 696) (SEQ. ID NO: 706)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 697) (SEQ. ID NO: 707)
5'- T GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 698) (SEQ. ID NO: 708)
20 5'- T GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 699) (SEQ. ID NO: 709)
5'- T GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 700) (SEQ. ID NO: 710)
5'- T GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 701) (SEQ. ID NO: 711)
5'- T GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 702) (SEQ. ID NO: 712)
5'- T GGA GGG CGG CAT GGC GGG CA-3' (FRAG 703) (SEQ. ID NO: 713)
25 5'- T GGA GGG CGG CAT GGC GGG C-3' (FRAG 704) (SEQ. ID NO: 714)
5'- T GGA GGG CGG CAT GGC GGG -3' (FRAG 705) (SEQ. ID NO: 715)
5'- T GGA GGG CGG CAT GGC GG-3' (FRAG 706) (SEQ. ID NO: 716)
5'- T GGA GGG CGG CAT GGC G-3' (FRAG 707) (SEQ. ID NO: 717)
5'- T GGA GGG CGG CAT GGC -3' (FRAG 708) (SEQ. ID NO: 718)
30 5'- T GGA GGG CGG CAT GG -3' (FRAG 709) (SEQ. ID NO: 719)
5'- T GGA GGG CGG CAT G -3' (FRAG 710) (SEQ. ID NO: 720)
5'- T GGA GGG CGG CAT -3' (FRAG 711) (SEQ. ID NO: 721)
5'- T GGA GGG CGG CA-3' (FRAG 712) (SEQ. ID NO: 722)
5'- T GGA GGG CGG C-3' (FRAG 713) (SEQ. ID NO: 723)
35 5'- T GGA GGG CGG -3' (FRAG 714) (SEQ. ID NO: 724)
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 715) (SEQ. ID NO: 725)
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 716) (SEQ. ID NO: 726)
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 717) (SEQ. ID NO: 727)
5'- GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 718) (SEQ. ID NO: 728)
40 5'- GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 719) (SEQ. ID NO: 729)
5'- GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 720) (SEQ. ID NO: 730)
5'- GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 721) (SEQ. ID NO: 731)
5'- GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 722) (SEQ. ID NO: 732)
5'- GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 723) (SEQ. ID NO: 733)
45 5'- GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 724) (SEQ. ID NO: 734)
5'- GGA GGG CGG CAT GGC GGG CA-3' (FRAG 725) (SEQ. ID NO: 735)
5'- GGA GGG CGG CAT GGC GGG C-3' (FRAG 726) (SEQ. ID NO: 736)
5'- GGA GGG CGG CAT GGC GGG -3' (FRAG 727) (SEQ. ID NO: 737)
5'- GGA GGG CGG CAT GGC GG-3' (FRAG 728) (SEQ. ID NO: 738)
50 5'- GGA GGG CGG CAT GGC G-3' (FRAG 729) (SEQ. ID NO: 739)
5'- GGA GGG CGG CAT GGC -3' (FRAG 730) (SEQ. ID NO: 740)
5'- GGA GGG CGG CAT GG -3' (FRAG 731) (SEQ. ID NO: 741)
5'- GGA GGG CGG CAT G -3' (FRAG 732) (SEQ. ID NO: 742)
5'- GGA GGG CGG CAT -3' (FRAG 733) (SEQ. ID NO: 743)
55 5'- GGA GGG CGG CA-3' (FRAG 734) (SEQ. ID NO: 744)
5'- GGA GGG CGG C-3' (FRAG 735) (SEQ. ID NO: 745)
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 736) (SEQ. ID NO: 746)
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 737) (SEQ. ID NO: 747)
5'- GA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 738) (SEQ. ID NO: 748)
60 5'- GA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 739) (SEQ. ID NO: 749)
5'- GA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 740) (SEQ. ID NO: 750)
5'- GA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 741) (SEQ. ID NO: 751)

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- 5'- GA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 742) (SEQ. ID NO: 752)
5'- GA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 743) (SEQ. ID NO: 753)
5'- GA GGG CGG CAT GGC GGG CAC A-3' (FRAG 744) (SEQ. ID NO: 754)
5'- GA GGG CGG CAT GGC GGG CAC-3' (FRAG 745) (SEQ. ID NO: 755)
5 5'- GA GGG CGG CAT GGC GGG CA-3' (FRAG 746) (SEQ. ID NO: 756)
5'- GA GGG CGG CAT GGC GGG C-3' (FRAG 747) (SEQ. ID NO: 757)
5'- GA GGG CGG CAT GGC GGG -3' (FRAG 748) (SEQ. ID NO: 758)
5'- GA GGG CGG CAT GGC GG-3' (FRAG 749) (SEQ. ID NO: 759)
5'- GA GGG CGG CAT GGC G-3' (FRAG 750) (SEQ. ID NO: 760)
10 5'- GA GGG CGG CAT GGC -3' (FRAG 751) (SEQ. ID NO: 761)
5'- GA GGG CGG CAT GG -3' (FRAG 752) (SEQ. ID NO: 762)
5'- GA GGG CGG CAT G -3' (FRAG 753) (SEQ. ID NO: 763)
5'- GA GGG CGG CAT -3' (FRAG 754) (SEQ. ID NO: 764)
5'- GA GGG CGG CA-3' (FRAG 755) (SEQ. ID NO: 765)
15 5'- A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 756) (SEQ. ID NO: 766)
5'- A GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 757) (SEQ. ID NO: 767)
5'- A GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 758) (SEQ. ID NO: 768)
5'- A GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 759) (SEQ. ID NO: 769)
5'- A GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 760) (SEQ. ID NO: 770)
20 5'- A GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 761) (SEQ. ID NO: 771)
5'- A GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 762) (SEQ. ID NO: 772)
5'- A GGG CGG CAT GGC GGG CAC AG-3' (FRAG 763) (SEQ. ID NO: 773)
5'- A GGG CGG CAT GGC GGG CAC A-3' (FRAG 764) (SEQ. ID NO: 774)
5'- A GGG CGG CAT GGC GGG CAC-3' (FRAG 765) (SEQ. ID NO: 775)
25 5'- A GGG CGG CAT GGC GGG CA-3' (FRAG 766) (SEQ. ID NO: 776)
5'- A GGG CGG CAT GGC GGG C-3' (FRAG 767) (SEQ. ID NO: 777)
5'- A GGG CGG CAT GGC GGG -3' (FRAG 768) (SEQ. ID NO: 778)
5'- A GGG CGG CAT GGC GG-3' (FRAG 769) (SEQ. ID NO: 779)
5'- A GGG CGG CAT GGC G-3' (FRAG 770) (SEQ. ID NO: 780)
30 5'- A GGG CGG CAT GGC -3' (FRAG 771) (SEQ. ID NO: 781)
5'- A GGG CGG CAT GG -3' (FRAG 772) (SEQ. ID NO: 782)
5'- A GGG CGG CAT G -3' (FRAG 773) (SEQ. ID NO: 783)
5'- A GGG CGG CAT -3' (FRAG 774) (SEQ. ID NO: 784)
5'- GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 775) (SEQ. ID NO: 785)
35 5'- GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 776) (SEQ. ID NO: 786)
5'- GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 777) (SEQ. ID NO: 787)
5'- GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 778) (SEQ. ID NO: 788)
5'- GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 779) (SEQ. ID NO: 789)
5'- GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 780) (SEQ. ID NO: 790)
40 5'- GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 781) (SEQ. ID NO: 791)
5'- GGG CGG CAT GGC GGG CAC AG-3' (FRAG 782) (SEQ. ID NO: 792)
5'- GGG CGG CAT GGC GGG CAC A-3' (FRAG 783) (SEQ. ID NO: 793)
5'- GGG CGG CAT GGC GGG CAC-3' (FRAG 784) (SEQ. ID NO: 794)
5'- GGG CGG CAT GGC GGG CA-3' (FRAG 785) (SEQ. ID NO: 795)
45 5'- GGG CGG CAT GGC GGG C-3' (FRAG 786) (SEQ. ID NO: 796)
5'- GGG CGG CAT GGC GGG -3' (FRAG 787) (SEQ. ID NO: 797)
5'- GGG CGG CAT GGC GG-3' (FRAG 788) (SEQ. ID NO: 798)
5'- GGG CGG CAT GGC G-3' (FRAG 789) (SEQ. ID NO: 799)
5'- GGG CGG CAT GGC -3' (FRAG 790) (SEQ. ID NO: 800)
50 5'- GGG CGG CAT GG -3' (FRAG 791) (SEQ. ID NO: 801)
5'- GGG CGG CAT G -3' (FRAG 792) (SEQ. ID NO: 802)
5'- GG CGG CAT GGC GGG CAC AG G CTG GGC-3' (FRAG 793) (SEQ. ID NO: 803)
5'- GG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 794) (SEQ. ID NO: 804)
5'- GG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 795) (SEQ. ID NO: 805)
55 5'- GG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 796) (SEQ. ID NO: 806)
5'- GG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 797) (SEQ. ID NO: 807)
5'- GG CGG CAT GGC GGG CAC AGG C-3' (FRAG 798) (SEQ. ID NO: 808)
5'- GG CGG CAT GGC GGG CAC AGG -3' (FRAG 799) (SEQ. ID NO: 809)
5'- GG CGG CAT GGC GGG CAC AG-3' (FRAG 800) (SEQ. ID NO: 810)
60 5'- GG CGG CAT GGC GGG CAC A-3' (FRAG 801) (SEQ. ID NO: 811)
5'- GG CGG CAT GGC GGG CAC-3' (FRAG 802) (SEQ. ID NO: 812)
5'- GG CGG CAT GGC GGG CA-3' (FRAG 803) (SEQ. ID NO: 813)

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- 5'- GG CGG CAT GGC GGG C-3' (FRAG 804) (SEQ. ID NO: 814)
5'- GG CGG CAT GGC GGG -3' (FRAG 805) (SEQ. ID NO: 815)
5'- GG CGG CAT GGC GG-3' (FRAG 806) (SEQ. ID NO: 816)
5'- GG CGG CAT GGC G-3' (FRAG 807) (SEQ. ID NO: 817)
5 5'- GG CGG CAT GGC -3' (FRAG 808) (SEQ. ID NO: 818)
5'- GG CGG CAT GG -3' (FRAG 809) (SEQ. ID NO: 819)
5'- G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 810) (SEQ. ID NO: 820)
5'- G CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 811) (SEQ. ID NO: 821)
5'- G CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 812) (SEQ. ID NO: 822)
10 5'- G CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 813) (SEQ. ID NO: 823)
5'- G CGG CAT GGC GGG CAC AGG CT-3' (FRAG 814) (SEQ. ID NO: 824)
5'- G CGG CAT GGC GGG CAC AGG C-3' (FRAG 815) (SEQ. ID NO: 825)
5'- G CGG CAT GGC GGG CAC AGG -3' (FRAG 816) (SEQ. ID NO: 826)
5'- G CGG CAT GGC GGG CAC AG-3' (FRAG 817) (SEQ. ID NO: 827)
15 5'- G CGG CAT GGC GGG CAC A-3' (FRAG 818) (SEQ. ID NO: 828)
5'- G CGG CAT GGC GGG CAC-3' (FRAG 819) (SEQ. ID NO: 829)
5'- G CGG CAT GGC GGG CA-3' (FRAG 820) (SEQ. ID NO: 830)
5'- G CGG CAT GGC GGG C-3' (FRAG 821) (SEQ. ID NO: 831)
5'- G CGG CAT GGC GGG -3' (FRAG 822) (SEQ. ID NO: 832)
20 5'- G CGG CAT GGC GG-3' (FRAG 823) (SEQ. ID NO: 833)
5'- G CGG CAT GGC G-3' (FRAG 824) (SEQ. ID NO: 834)
5'- G CGG CAT GGC -3' (FRAG 825) (SEQ. ID NO: 835)
5'- CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 826) (SEQ. ID NO: 836)
5'- CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 827) (SEQ. ID NO: 837)
25 5'- CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 828) (SEQ. ID NO: 838)
5'- CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 829) (SEQ. ID NO: 839)
5'- CGG CAT GGC GGG CAC AGG CT-3' (FRAG 830) (SEQ. ID NO: 840)
5'- CGG CAT GGC GGG CAC AGG C-3' (FRAG 831) (SEQ. ID NO: 841)
5'- CGG CAT GGC GGG CAC AGG -3' (FRAG 832) (SEQ. ID NO: 842)
30 5'- CGG CAT GGC GGG CAC AG-3' (FRAG 833) (SEQ. ID NO: 843)
5'- CGG CAT GGC GGG CAC A-3' (FRAG 834) (SEQ. ID NO: 844)
5'- CGG CAT GGC GGG CAC-3' (FRAG 835) (SEQ. ID NO: 845)
5'- CGG CAT GGC GGG CA-3' (FRAG 836) (SEQ. ID NO: 846)
5'- CGG CAT GGC GGG C-3' (FRAG 837) (SEQ. ID NO: 847)
35 5'- CGG CAT GGC GGG -3' (FRAG 838) (SEQ. ID NO: 848)
5'- CGG CAT GGC GG-3' (FRAG 839) (SEQ. ID NO: 849)
5'- CGG CAT GGC G-3' (FRAG 840) (SEQ. ID NO: 850)
5'- GG CAT GGC GGG CAC AGG C TG GGC-3' (FRAG 841) (SEQ. ID NO: 851)
5'- GG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 842) (SEQ. ID NO: 852)
40 5'- GG CAT GGC GGG CAC AGG CTG G-3' (FRAG 843) (SEQ. ID NO: 853)
5'- GG CAT GGC GGG CAC AGG CTG -3' (FRAG 844) (SEQ. ID NO: 854)
5'- GG CAT GGC GGG CAC AGG CT-3' (FRAG 845) (SEQ. ID NO: 855)
5'- GG CAT GGC GGG CAC AGG C-3' (FRAG 846) (SEQ. ID NO: 856)
5'- GG CAT GGC GGG CAC AGG -3' (FRAG 847) (SEQ. ID NO: 857)
45 5'- GG CAT GGC GGG CAC AG-3' (FRAG 848) (SEQ. ID NO: 858)
5'- GG CAT GGC GGG CAC A-3' (FRAG 849) (SEQ. ID NO: 859)
5'- GG CAT GGC GGG CAC-3' (FRAG 850) (SEQ. ID NO: 860)
5'- GG CAT GGC GGG CA-3' (FRAG 851) (SEQ. ID NO: 861)
5'- GG CAT GGC GGG C-3' (FRAG 852) (SEQ. ID NO: 862)
50 5'- GG CAT GGC GGG -3' (FRAG 853) (SEQ. ID NO: 863)
5'- GG CAT GGC GG-3' (FRAG 854) (SEQ. ID NO: 864)
5'- G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 855) (SEQ. ID NO: 865)
5'- G CAT GGC GGG CAC AGG CTG GG-3' (FRAG 856) (SEQ. ID NO: 866)
5'- G CAT GGC GGG CAC AGG CTG G-3' (FRAG 857) (SEQ. ID NO: 867)
55 5'- G CAT GGC GGG CAC AGG CTG -3' (FRAG 858) (SEQ. ID NO: 868)
5'- G CAT GGC GGG CAC AGG CT-3' (FRAG 859) (SEQ. ID NO: 869)
5'- G CAT GGC GGG CAC AGG C-3' (FRAG 860) (SEQ. ID NO: 870)
5'- G CAT GGC GGG CAC AGG -3' (FRAG 861) (SEQ. ID NO: 871)
5'- G CAT GGC GGG CAC AG-3' (FRAG 862) (SEQ. ID NO: 872)
60 5'- G CAT GGC GGG CAC A-3' (FRAG 863) (SEQ. ID NO: 873)
5'- G CAT GGC GGG CAC-3' (FRAG 864) (SEQ. ID NO: 874)
5'- G CAT GGC GGG CA-3' (FRAG 865) (SEQ. ID NO: 875)

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- 5'- G CAT GGC GGG C-3' (FRAG 866) (SEQ. ID NO: 876)
5'- G CAT GGC GGG -3' (FRAG 867) (SEQ. ID NO: 877)
5'- CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 868) (SEQ. ID NO: 878)
5'- CAT GGC GGG CAC AGG CTG GG-3' (FRAG 869) (SEQ. ID NO: 879)
5 CAT 5'- CAT GGC GGG CAC AGG CTG G-3' (FRAG 870) (SEQ. ID NO: 880)
5'- CAT GGC GGG CAC AGG CTG -3' (FRAG 871) (SEQ. ID NO: 881)
5'- CAT GGC GGG CAC AGG CT-3' (FRAG 872) (SEQ. ID NO: 882)
5'- CAT GGC GGG CAC AGG C-3' (FRAG 873) (SEQ. ID NO: 883)
5'- CAT GGC GGG CAC AGG -3' (FRAG 874) (SEQ. ID NO: 884)
10 5'- CAT GGC GGG CAC AG-3' (FRAG 875) (SEQ. ID NO: 885)
5'- CAT GGC GGG CAC A-3' (FRAG 876) (SEQ. ID NO: 886)
5'- CAT GGC GGG CAC-3' (FRAG 877) (SEQ. ID NO: 887)
5'- CAT GGC GGG CA-3' (FRAG 878) (SEQ. ID NO: 888)
5'- CAT GGC GGG C-3' (FRAG 879) (SEQ. ID NO: 889)
15 5'- AT GGC GGG CAC AGG CTG GGC-3' (FRAG 880) (SEQ. ID NO: 890)
5'- AT GGC GGG CAC AGG CTG GG-3' (FRAG 881) (SEQ. ID NO: 891)
5'- AT GGC GGG CAC AGG CTG G-3' (FRAG 882) (SEQ. ID NO: 892)
5'- AT GGC GGG CAC AGG CTG -3' (FRAG 883) (SEQ. ID NO: 893)
5'- AT GGC GGG CAC AGG CT-3' (FRAG 884) (SEQ. ID NO: 894)
20 5'- AT GGC GGG CAC AGG C-3' (FRAG 885) (SEQ. ID NO: 895)
5'- AT GGC GGG CAC AGG -3' (FRAG 886) (SEQ. ID NO: 896)
5'- AT GGC GGG CAC AG-3' (FRAG 887) (SEQ. ID NO: 897)
5'- AT GGC GGG CAC A-3' (FRAG 888) (SEQ. ID NO: 898)
5'- AT GGC GGG CAC-3' (FRAG 889) (SEQ. ID NO: 899)
25 5'- AT GGC GGG CA-3' (FRAG 890) (SEQ. ID NO: 900)
5'- T GGC GGG CAC AGG CTG GGC-3' (FRAG 891) (SEQ. ID NO: 901)
5'- T GGC GGG CAC AGG CTG GG-3' (FRAG 892) (SEQ. ID NO: 902)
5'- T GGC GGG CAC AGG CTG G-3' (FRAG 893) (SEQ. ID NO: 903)
5'- T GGC GGG CAC AGG CTG -3' (FRAG 894) (SEQ. ID NO: 904)
30 5'- T GGC GGG CAC AGG CT-3' (FRAG 895) (SEQ. ID NO: 905)
5'- T GGC GGG CAC AGG C-3' (FRAG 896) (SEQ. ID NO: 906)
5'- T GGC GGG CAC AGG -3' (FRAG 897) (SEQ. ID NO: 907)
5'- T GGC GGG CAC AG-3' (FRAG 898) (SEQ. ID NO: 908)
5'- T GGC GGG CAC A-3' (FRAG 899) (SEQ. ID NO: 909)
35 5'- T GGC GGG CAC-3' (FRAG 900) (SEQ. ID NO: 910)
5'- GGC GGG CAC AGG CTG GGC-3' (FRAG 901) (SEQ. ID NO: 911)
5'- GGC GGG CAC AGG CTG GG-3' (FRAG 902) (SEQ. ID NO: 912)
5'- GGC GGG CAC AGG CTG G-3' (FRAG 903) (SEQ. ID NO: 913)
5'- GGC GGG CAC AGG CTG -3' (FRAG 904) (SEQ. ID NO: 914)
40 5'- GGC GGG CAC AGG CT-3' (FRAG 905) (SEQ. ID NO: 915)
5'- GGC GGG CAC AGG C-3' (FRAG 906) (SEQ. ID NO: 916)
5'- GGC GGG CAC AGG -3' (FRAG 907) (SEQ. ID NO: 917)
5'- GGC GGG CAC AG-3' (FRAG 908) (SEQ. ID NO: 918)
5'- GGC GGG CAC A-3' (FRAG 909) (SEQ. ID NO: 919)
45 5'- GC GGG CAC AGG CTG GGC-3' (FRAG 910) (SEQ. ID NO: 920)
5'- GC GGG CAC AGG CTG GG-3' (FRAG 911) (SEQ. ID NO: 921)
5'- GC GGG CAC AGG CTG G-3' (FRAG 912) (SEQ. ID NO: 922)
5'- GC GGG CAC AGG CTG -3' (FRAG 913) (SEQ. ID NO: 923)
5'- GC GGG CAC AGG CT-3' (FRAG 914) (SEQ. ID NO: 924)
50 5'- GC GGG CAC AGG C-3' (FRAG 915) (SEQ. ID NO: 925)
5'- GC GGG CAC AGG -3' (FRAG 916) (SEQ. ID NO: 926)
5'- GC GGG CAC AG-3' (FRAG 917) (SEQ. ID NO: 927)
5'- C GGG CAC AGG CTG GGC-3' (FRAG 918) (SEQ. ID NO: 928)
5'- GGG CAC AGG CTG GG-3' (FRAG 919) (SEQ. ID NO: 929)
55 5'- C GGG CAC AGG CTG G-3' (FRAG 920) (SEQ. ID NO: 930)
5'- C GGG CAC AGG CTG -3' (FRAG 921) (SEQ. ID NO: 931)
5'- C GGG CAC AGG CT-3' (FRAG 922) (SEQ. ID NO: 932)
5'- C GGG CAC AGG C-3' (FRAG 923) (SEQ. ID NO: 933)
5'- C GGG CAC AGG -3' (FRAG 924) (SEQ. ID NO: 934)
60 5'- GGG CAC AGG CTG GGC-3' (FRAG 925) (SEQ. ID NO: 935)
5'- GGG CAC AGG CTG GG-3' (FRAG 926) (SEQ. ID NO: 936)
5'- GGG CAC AGG CTG G-3' (FRAG 927) (SEQ. ID NO: 937)

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- 5'- GGG CAC AGG CTG -3' (FRAG 928) (SEQ. ID NO: 938)
 5'- GGG CAC AGG CT-3' (FRAG 929) (SEQ. ID NO: 939)
 5'- GGG CAC AGG C-3' (FRAG 930) (SEQ. ID NO: 940)
 5'- GG CAC AGG CTG GGC-3' (FRAG 931) (SEQ. ID NO: 941)
 5 5'- GG CAC AGG CTG GG-3' (FRAG 932) (SEQ. ID NO: 942)
 5'- GG CAC AGG CTG G-3' (FRAG 933) (SEQ. ID NO: 943)
 5'-GG CAC AGG CTG -3' (FRAG 934) (SEQ. ID NO: 944)
 5'- GG CAC AGG CT-3' (FRAG 935) (SEQ. ID NO: 945)
 5'-G CAC AGG CTG GGC-3' (FRAG 936) (SEQ. ID NO: 946)
 10 5'-G CAC AGG CTG GG-3' (FRAG 937) (SEQ. ID NO: 947)
 5'-G CAC AGG CTG G-3' (FRAG 938) (SEQ. ID NO: 948)
 5'-G CAC AGG CTG -3' (FRAG 939) (SEQ. ID NO: 949)
 5'-CAC AGG CTG GGC-3' (FRAG 940) (SEQ. ID NO: 950)
 5'-CAC AGG CTG GG-3' (FRAG 941) (SEQ. ID NO: 951)
 15 5'-CAC AGG CTG G-3' (FRAG 942) (SEQ. ID NO: 952)
 5'-AC AGG CTG GGC-3' (FRAG 943) (SEQ. ID NO: 953)
 5'-AC AGG CTG GG-3' (FRAG 944) (SEQ. ID NO: 954)
 5'-C AGG CTG GGC-3' (FRAG 945) (SEQ. ID NO: 955)
 5'-TTT TCC TTC CTT TGT CTC TCT TC (FRAG 946) (SEQ. ID NO: 956)
 20 5'-GCT CCC GGC TGC CTG (FRAG 947) (SEQ. ID NO: 957)
 5'-CTC GGC CGT GCG GCT CTG TCG CTC CCG GT (FRAG 948) (SEQ. ID NO: 958)
 5'-CCG CCG CCC TCC GGG GGG TC (FRAG 949) (SEQ. ID NO: 959)
 5'-TGC TGC CGT TGG CTG CCC (FRAG 950) (SEQ. ID NO: 960)
 5'-CTT CTG CGG GTC GCC GG (FRAG 951) (SEQ. ID NO: 961)
 25 5'-TGC TGG GCT TGT GGC (FRAG 952) (SEQ. ID NO: 962)
 5'-GGC CTC TCT TCT GGG (FRAG 953) (SEQ. ID NO: 963)
 5'-CCT GGT CCC TCC GT (FRAG 954) (SEQ. ID NO: 964)
 5'-GGT GGC TCC TCT GC (FRAG 955) (SEQ. ID NO: 965)
 5'-GCT TGG TCC TGG GGC TGC (FRAG 956) (SEQ. ID NO: 966)
 30 5'-TGC TCT CCT CTC CTT (FRAG 957) (SEQ. ID NO: 967)

Human Adenosine A2a Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-TGC TTT TCT TTT CTG GGC CTC TGT GGT CTG TTT TTT TCT G GCC CTG CTG GGG CGC TCT CC GCC GCC
 CGC CTG GCT CCC GGB GCC CBT GBT GGG CBT GCC GTG GTT CTT GCC CTC CTT TGG CTG CCG TGC CCG CTC
 CCC GGC CTC CTG GCG GGT GGC CGT TG GGC CCG TGT TCC CCT GGG -GCC TGG GGC TCC CTT CTC TC GCC
 35 CTT CTT GCT GGG-CCT C TGC TGC TGC TGG TGC TGT GGC CCC C GTA CAC CGA GGA GCC CAT GAT GGG CAT
 GCC ACA GAC GAC AGG C GTB CBC CGB GGB GCC CBT GBT GGG CBT GCC BCB GBC GBC BGG C-3' (FRAG. NO.
 1665) (SEQ. ID NO:1680)
 5'-CTG GGC CTC-3' (FRAG 1666) (SEQ. ID NO: 1681)
 5'-TGC TTT TCT TTT CTG GGC CTC-3' (FRAG 958) (SEQ. ID NO: 968)
 40 5'-TGT GGT CTG TTT TTT TCT G-3' (FRAG 959) (SEQ. ID NO: 969)
 5'-GCC CTG CTG GGG CGC TCT CC-3' (FRAG 960) (SEQ. ID NO: 970)
 5'-GCC GCC CGC CTG GCT CCC-3' (FRAG 961) (SEQ. ID NO: 971)
 5'-GGB GCC CBT GBT GGG CBT GCC-3' (FRAG 962) (SEQ. ID NO: 972)
 5'-GTG GTT CTT GCC CTC CTT TGG CTG-3' (FRAG 963) (SEQ. ID NO: 973)
 45 5'-CCG TGC CCG CTC CCC GGC-3' (FRAG 964) (SEQ. ID NO: 974)
 5'-CTC CTG GCG GGT GGC CGT TG-3' (FRAG 965) (SEQ. ID NO: 975)
 5'-GGC CCG TGT TCC CCT GGG-3' (FRAG 966) (SEQ. ID NO: 976)
 5'-GCC TGG GGC TCC CTT CTC TC-3' (FRAG 967) (SEQ. ID NO: 977)

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5 GAGGCGCGGT CCGGGCGCTA TGGCCATGCC CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GGCGCGCCTT
 CGGTAGGGGG CGCCCGGGGC CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC
 GCTGGAGCTG GTCATCGCCG CGCTTTCGGT GCGGGGCAAC GTGCTGGTGT GCGCCGCGGT GGGCACGGCG
 AACACTCTGC AGACGCCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC GTGGGGCTCT
 TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TCTTCCTCGC
 CTGCTTCGTG CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTCTGGCCG TGGCAGTCGA CAGATACCTG
 GCCATCTGTG TCCCGCTCAG GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC
 TCTGGGTCTT TGCCTTTGGC ATCGGATTGA CTCCATTCTT GGGGTGGAAC AGTAAAGACA GTGCCACCAA
 CAACTGCACA GAACCCTGGG ATGGAACCAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT
 10 GTGGTCCCA TGAGCTACAT GGTATATTTC AATTCTTTG GGTGTGTCTT GGTGTGTCTT CTTATAATGC
 TGGTGATCTA CATTAAAGATC TTCTGGTGG CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA TGGACCACTC
 GAGGACCACC CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGCCCTG
 TGCTGGTTAC CTGTGCATGC TGTTAACTGT GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA
 AGTGGGCAAT GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATTG TCTATGCTTA
 15 CCGGAACCGA GACTTCCGCT ACACCTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC
 AAGAGTGGGA ATGTCAGGC TGGGGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG CTCTCGCCTC
 TTCCAGGAGA AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT TTCATTGTGA AAGATAGCTA
 CACCTCACAA GGAATGGAC TGCCTCTCTT GAGCACTTCC CTGGAGCTAC CACGTATCTA GCTAATATGT
 ATGTGTCAGT AGTAGCACC AAGATTGACA AATATATTTA TGATCTATTC AGCTGCTTTT ACTGTGTGGA
 20 TTATGCCAAC AGCTTGAATG GATTCTAACA GACTCTTTTG TTTTAAAAAG TCTGCCTTGT TTATGGTGGA
 AAATTACTGA AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTT AACTTAGAGG
 AATAGGAAAA ATAAAAGTTG ATGTACTAA AAATGTATAC TTGTGCCCAG GAAGGTGACC TCAAAAATTA
 AAAGTATAAT TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG
 GCGGATCACG AGGTCAGGAG TTCAAAACCA GCCTGTCCAA TATAGTG GGGCAATTG TTAGTTATCC
 25 GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGAGGGG CCCGCGCGG GCGCGAACTT TGGGCTCGGG
 CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTTGCCCG
 CGGGGGGCCC CGACCCGTGG GTCCCGGCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG
 GCGCGGTCCG GCGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCC CTCGCCCCGGC GCGCCTTCGG
 TAGGGGGGCG CCGGGGCCCA GCTGGCCCG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT
 30 GGAGCTGGTC ATCGCCGCGC TTTCGGTGGC GGGCAACGTG CTGGTGTGCG CCGCGGTGGG CACGGCGAAC
 ACTCTGCAGA CGCCACCAA CTACTTCTG GTGTCCCTGG CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG
 CCATCCCCTT TGCCATCACC ATCAGCCTGG GCTTCTGCAC TGACTTCTAC GGCTGCCTCT TCCTCGCCTG
 CTTCTGTGCT GTGCTCACGC AGAGCTCCAT CTTACGCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC
 ATCTGTGTCC CGCTCAGGTA TAAAAGTTT GTACGGGGA CCCGAGCAAG AGGGGTCAAT GCTGTCTCT
 35 GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCTGGG GTGGAACAGT AAAGACAGT CCACCAACA
 CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCTTGTGA ATGTCTCTT TGAGAATGTG
 GTCCCATGA GCTACATGGT ATATTCAAT TTCTTTGGGT GTGTCTGCC CCCACTGCTT ATAATGCTGG
 TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG
 GACCACCCTC CAGCGGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC
 40 TGGTTACCTG TGCATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT
 GGGCAATGAA TATGGCCATT CTTCTGTAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT ATGCTTACCG
 GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC TCTGCCAAGC AGATGTCAAG
 AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG ATCTAGGCTC TCGCCTCTTC
 CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTTC ATTGTGAAAG ATAGCTACAC
 45 CTCACAAGGA AATGGACTGC CTCTCTTGG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG
 TGTCAGTAGT AGGCTCCAAG GATTGACAAA TATATTATG ATCTATTAG CTGCTTTTAC TGTGTGGATT
 ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGT TTTAAAAGTC TGCCTTGTTC ATGGTGGA
 ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACATTT ATAATGCAAA TACTTTTAA CTTAGAGGCA
 ATGGA AAAAGTTGAC TGTAATAAAA ATG CCCAGCCCCG AGGCTCAGAA GCGGCAGGCG GAGGCGCGGT
 50 CCGGGCGCTA TGGCCATGCC CGGCGGGTCT CACGCGGCTG CCCCTCGCCC GGCGCGCCTT CGGTAGGGGG
 CGCCCGGGGC CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC GCTGGAGCTG
 GTCATCGCCG CGCTTTCGGT GCGGGGCAAC GTGCTGGTGT GCGCCGCGGT GGGCACGGCG AACACTCTGC
 AGACGCCAC CAACTACTTC CTGGTGTCCC TGGCTGCGGC CGACGTGGCC GTGGGGCTCT TCGCCATCCC
 CTTTGCCATC ACCATCAGCC TGGGCTTCTG CACTGACTTC TACGGCTGCC TCTTCCTCGC CTGCTTCGTG
 55 CTGGTGCTCA CGCAGAGCTC CATCTTCAGC CTTCTGGCCG TGGCAGTCGA CAGATACCTG GCCATCTGTG
 TCCCGCTCAG GTATAAAAGT TTGGTCACGG GGACCCGAGC AAGAGGGGTC ATTGCTGTCC TCTGGGTCTT
 TGCCTTTGGC ATCGGATTGA CTCCATTCTT GGGGTGGAAC AGTAAAGACA GTGCCACCAA CAACTGCACA
 GAACCCTGGG ATGGAACCAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT CTTTGAGAAT GTGGTCCCA
 TGAGCTACAT GGTATATTTC AATTCTTTG GGTGTGTCTT GCGCCCACTG CTTATAATGC TGGTGATCTA

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CATTAAGATC TTCCTGGTGG CCTGCAGGCA GCTTCAGCGC ACTGAGCTGA TGGACCACTC GAGGACCACC
 CTCCAGCGGG AGATCCATGC AGCCAAGTCA CTGGCCATGA TTGTGGGGAT TTTTGGCCCTG TGCTGGTTAC
 CTGTGCATGC TGTTAACTGT GTCACTCTTT TCCAGCCAGC TCAGGGTAAA AATAAGCCCA AGTGGGCAAT
 GAATATGGCC ATTCTTCTGT CACATGCCAA TTCAGTTGTC AATCCCATTG TCTATGCTTA CCGGAACCGA
 5 GACTTCCGCT ACACTTTTCA CAAAATTATC TCCAGGTATC TTCTCTGCCA AGCAGATGTC AAGAGTGGGA
 ATGGTCAGGC TGGGGTACAG CCTGCTCTCG GTGTGGGCCT ATGATCTAGG CTCTCGCCTC TTCCAGGAGA
 AGATACAAAT CCACAAGAAA CAAAGAGGAC ACGGCTGGTT TTCATTGTGA AAGATAGCTA CACCTCACAA
 GGAAATGGAC TGCCTCTCTT GAGCACTTCC CTGGAGCTAC CACGTATCTA GCTAATATGT ATGTGTCACT
 AGTAGCACCA AGGATTGACA AATATAATTA TGATCTATTC AGCTGCTTTT ACTGTGTGGA TTATGCCAAC
 10 AGCTTGAATG GATTCTAACA GACTCTTTTG TTTTAAAAAG TCTGCCTTGT TTATGGTGGGA AAATTACTGA
 AACTATTTTA CTGTGAAACA GTGTGAACTA TTATAATGCA AATACTTTT AACTTAGAGG CAATGGAAAA
 ATAAAAGTTG ACTGTACTAA AAATGTATAC TTGTTGCCAG GAAGGTGACC TCAAAAATTA AAAGTATAAT
 TATTCGGCCG GGCATGGTGG CTCACACCTG TAATTCCAGC ACTTTGGGAG GCCAAGGCAG GCGGATCACG
 AGGTACAGGAG TTCAAAAACCA GCCTGTCCAA TATAGTG GGGCAATTTG TTAGTTATCC GCCGCCACCA
 15 AGACGCGGCA CGGCGCCTGG ACCGAGGGG CCGCGCGCG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG
 GTGCTCCGCC CAGCCCGAGA CGGGCGGGCG CGCGGGCCAA TGGGTGCCGC CTCTGGCCG CCGGGGGCCC
 CGACCCGTGG GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG
 GCGCTATGG CCATGCCCCG CGGGTCTCAC GCGGTGCCC CTCGCCCCGC GCGCCTTCGG TGGGGGCGC
 CCGGGGCCA GCTGGCCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT ACGTGGCGCT GGAGTGGTC
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5'-GCCGCTCCTG-3' (FRAG. NO: 1671) (SEQ. ID NO: 1686)

5'-GCT GGG CCC CGG-3' (FRAG. NO: 1672) (SEQ. ID NO: 1687)

5'-CGG GTC GGG GCC CCC C-3' (FRAG. NO: 1673) (SEQ. ID NO: 1688)

25 5'-CGC GCC CGC G-3' (FRAG. NO: 1674) (SEQ. ID NO: 1689)

5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG-3' (FRAG 972) (SEQ. ID NO: 982)

5'-GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC-3' (FRAG 973) (SEQ. ID NO: 983)

5'-GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC-3' (FRAG 974) (SEQ. ID NO: 984)

5'-CGG GTC GGG GCC CCC CGC GGC C-3' (FRAG 975) (SEQ. ID NO: 985)

30 5'-GCC TCG GGG CTG GGG CGC TGG TGG CCG GG-3' (FRAG 976) (SEQ. ID NO: 986)

5'-CCG CGC CTC CGC CTG CCG CTT CTG-3' (FRAG 977) (SEQ. ID NO: 987)

5'-GCT GGG CCC CGG GCG CCC CCT-3' (FRAG 978) (SEQ. ID NO: 988)

5'-CCC CTC TTG CTC GGG TCC CCG TG-3' (FRAG 979) (SEQ. ID NO: 989)

5'-ACAGCGCGTCTGTGTCTCCAGCAGCATGGCCGGGCCAGCTGGGCCCC-3' (FRAG 980) (SEQ. ID NO: 990)

35 5'-BCBGCGCGTCTGTGTCTCCBGCBGCBTGGCCGGGCCBGTGGGCCCC-3' (FRAG 981) (SEQ. ID NO: 991)

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 5'-GBG CB TGC-3' (FRAG. NO: 1676) (SEQ. ID NO: 1691)
 5'-TTG TTG GGC-3' (FRAG. NO: 1677) (SEQ. ID NO: 1692)
 5'-TGC CTT CCC BGG G-3' (FRAG. NO: 1678) (SEQ. ID NO: 1693)
 20 5'-GTT GTT GGG CAT CTT GCC-3' (FRAG. NO: 1679) (SEQ. ID NO: 3)
 5'-GTG GGC CTA GCT CTC GCC-3' (FRAG. NO: 1680) (SEQ. ID NO: 5)
 5'-ACA GAG CA TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G-3' (FRAG 982) (SEQ. ID NO: 992)
 5'-BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG G-3' (FRAG 983) (SEQ. ID NO: 993)
 5'-CCC TTT TCT GGT GGG GTG-3' (FRAG 984) (SEQ. ID NO: 994)
 25 5'-GTG CTG TTG TTG GGC-3' (FRAG 985) (SEQ. ID NO: 995)
 5'-TTT CTT CTG TTC CC-3' (FRAG 986) (SEQ. ID NO: 996)
 5'-CCC TTT TCT GGT GGG GTG-3' (FRAG 987) (SEQ. ID NO: 997)
 5'-GTG CTG TTG TTG GGC-3' (FRAG 988) (SEQ. ID NO: 998)
 5'-TTT CTT CTG TTC CC-3' (FRAG 989) (SEQ. ID NO: 999)
 30 **Human IgE Receptor β Nucleic Acid and Antisense Oligonucleotide Fragments**
 5'-TTT CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT
 TTC ATT AAC CGA GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT-3'
 (FRAG. NO: 1681) (SEQ. ID NO: 1694)
 5'-CCC CTG GG-3' (FRAG. NO: 1682) (SEQ. ID NO: 1695)
 35 5'-GCTCTCCTBTT-3' (FRAG. NO: 1683) (SEQ. ID NO: 1696)
 5'-CBTTBCCGBGCTG-3' (FRAG. NO: 1684) (SEQ. ID NO: 1697)
 5'-TTT CCC CTG GGT CTT CC-3' (FRAG 990) (SEQ. ID NO: 1000)
 5'-CTC CTG CTC TTT TTT C-3' (FRAG 991) (SEQ. ID NO: 1001)
 ATTTGCTCTCCTATTACTTTCTGTGTCCATTTTTCATTAACCGAGCTGT (FRAG 992) (SEQ. ID NO: 1002)
 40 BTTTGCTCTCCTBTTBCTTTCTGTGTCCBTTTTCBTTBCCGBGCTGT (FRAG 993) (SEQ. ID NO: 1003)
**Human Fc ϵ Receptor CD23 Antigen (IgE Receptor)
 Nucleic Acid and Antisense Oligonucleotide Fragments**
 5'-GCC TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC
 CGG GCT GTG G GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG
 45 C GGG TCT TGC TCT GGG CCT GGC TGT GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC TCT
 CTG AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA TCT CTG BBT BTT GBC CTT CCT
 CCB TGG CGG TCC TGC TTG GBT TCT CCC GB-3' (FRAG 1685) (SEQ. ID NO: 1698)
 5'-GT CCT CCT-3' (FRAG 1686) (SEQ. ID NO: 1699)
 5'-TGT GTC TGT CCT CC-3' (FRAG 1687) (SEQ. ID NO: 1700)
 50 5'-GTG GCC CTG GC-3' (FRAG 1688) (SEQ. ID NO: 1701)
 5'-CGT GGT TGG GG-3' (FRAG 1689) (SEQ. ID NO: 1702)
 5'-TCT CTG BBT BTT GBC C-3' (FRAG 1690) (SEQ. ID NO: 1703)
 5'-GCC TGT GTC TGT CCT CCT-3' (FRAG 994) (SEQ. ID NO: 1004)
 5'-GCT TCG TTC CTC TCG TTC-3' (FRAG 995) (SEQ. ID NO: 1005)
 55 5'-CTG CTT GGT GCC CTT GCC G-3' (FRAG 996) (SEQ. ID NO: 1006)
 5'-GTC CTG CTC CTC CGG GCT GTG G-3' (FRAG 997) (SEQ. ID NO: 1007)
 5'-GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG-3' (FRAG 998) (SEQ. ID NO: 1008)
 5'-CCT TCG CTG GCT GGC GGC GTG C-3' (FRAG 999) (SEQ. ID NO: 1009)

5'-GGG TCT TGC TCT GGG CCT GGC TGT-3' (FRAG 1000) (SEQ. ID NO: 1010)

5'-GGC CGT GGT TGG GGG TCT TC-3' (FRAG 1001) (SEQ. ID NO: 1011)

5'-GCT GCC TCC GTT TGG GTG GC (FRAG 1002) (SEQ. ID NO: 1012)

5'-TCT CTG AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA (FRAG 1003) (SEQ. ID NO: 1013)

5'-TCT CTG BBT BTT GBC CTT CCT CCB TGG CGG TCC TGC TTG GBT TCT CCC GB (FRAG 1004) (SEQ. ID NO: 1014)

Human IgE Receptor α Subunit Nucleic Acid and Antisense Oligonucleotide Fragments

5'- GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT ACA GTA GAG TAG GGG ATT CCA TGG CAG
GAG CCA TCT TCT TCA TGG ACT CC TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT
GGA GC BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC
10 TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GTT GTT TTT GGG GTT TGG CTT GCC TTT CCT
GGT TCT CTT BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG
BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO: 1691) (SEQ. ID NO: 1704)
5'- TGG BCT CC -3' (FRAG. NO: 1692) (SEQ. ID NO: 1705)
5'-CCB TCT GGB-3' (FRAG. NO: 1693) (SEQ. ID NO: 1706)
15 5'-CT GCT BBC BCG-3' (FRAG. NO: 1694) (SEQ. ID NO: 1707)
5'-GTT TTT GGG GTT TG-3' (FRAG. NO: 1695) (SEQ. ID NO: 1708)
5'-GCC TTT CCT GGT TCT CTT GTT GTT TTT GGG GTT TGG CTT-3' (FRAG. NO: 1005) (SEQ. ID NO: 1015)
5'-ACAGTAGAGTAGGGGATTCCATGGCAGGAGCCATCTTCTTCATGGACTCC-3' (FRAG. NO: 1006) (SEQ. ID NO: 1016)
5'-TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT GGA GC-3' (FRAG. NO: 1007) (SEQ.
20 ID NO: 1017)
5'-BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT TCB TGG BCT CC TTC BBG GBG BCC TTB GGT
TTC TGB GGG-3' (FRAG. NO: 1008) (SEQ. ID NO: 1018)
5'-BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO: 1009) (SEQ. ID NO: 1019)
5'-GTT GTT TTT GGG GTT TGG CTT-3' (FRAG. NO: 1010) (SEQ. ID NO: 1020)
25 5'-GCC TTT CCT GGT TCT CTT-3' (FRAG. NO: 1011) (SEQ. ID NO: 1021)
5'-BCBGTBGBGTBGGGGBTTCBTTGGCBGGBGCCBTCTTCTTCBTGGBCTCC-3' (FRAG. NO: 1012) (SEQ. ID NO: 1022)
5'-TTC BBG GBG BCC TTB GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO: 1013) (SEQ. ID
NO: 1023)

Human IgE Receptor (Fc Epsilon R) Nucleic Acid and Antisense Oligonucleotide Fragments

30 5'-GCC TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC
CGG GCT GTG G GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C
CCC BGB BCG BGB CCC GGB CCG BCB GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC GAT
CTC TGA ATA TTGA CCT TCC ATG GCG GTC CTG CTT GGA GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC
CTG CTT GGB-3' (FRAG: 1696) (SEQ. ID NO: 1709)
35 5'-TCG TTC CTC TCG-3' (FRAG: 1697) (SEQ. ID NO: 3001)
5'-BGB BCG BGB C-3' (FRAG: 1698) (SEQ. ID NO: 1711)
5'-TGB BTB TTGB-3' (FRAG: 1699) (SEQ. ID NO: 1712)
5'-GCC TGT GTC TGT CCT CCT-3' (FRAG. NO: 1014) (SEQ. ID NO: 1024)
5'-GCT TCG TTC CTC TCG TTC-3' (FRAG. NO: 1015) (SEQ. ID NO: 1025)
40 5'-CTG CTT GGT GCC CTT GCC G-3' (FRAG. NO: 1016) (SEQ. ID NO: 1026)
5'-GTC CTG CTC CTC CGG GCT GTG G-3' (FRAG. NO: 1017) (SEQ. ID NO: 1027)
5'-GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG-3' (FRAG. NO: 1018) (SEQ. ID NO: 1028)
5'-CCT TCG CTG GCT GGC GGC GTG C-3' (FRAG. NO: 1019) (SEQ. ID NO: 1029)
5'-CCC BGB BCG BGB CCC GGB CCG BCB-3' (FRAG. NO: 1020) (SEQ. ID NO: 1030)
45 5'-GGC CGT GGT TGG GGG TCT TC-3' (FRAG. NO: 1021) (SEQ. ID NO: 1031)
5'-GCT GCC TCC GTT TGG GTG GC-3' (FRAG. NO: 1022) (SEQ. ID NO: 1032)
5'-GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB-3' (FRAG. NO: 1023) (SEQ. ID NO: 1033)

Human High Affinity IgE Receptor Oligonucleotide Fragments

5'-AACAAGAAAA GCGTTGGTAG CTCTGGTGAA TCCCAAAAGA ATGTGGCAGT TGCTAGCCAT GCTCCTGAAT
50 ATGTATAAAC AGTACATCAT ATGACTAAGA GTTTGACTTA GGGGTTAGAT TTTATGTGTT TGAACCCCAA
ATTAGTTATT TAATAGTTGG CACCCCAAAA CAAGTTACTT AACCTCACTA AGGTTCAAGT TTCCTGTTTA
TAAAATGTAG ATAGTGATAG TATGTACTTT ATAGGATTAT TGTGAAAAAT AAATGAAATA TCAGATTTAT
TTAGGATAAC ACCTGGCATA TGTTTGGTAT TCAGAATTAG TTGCTGCTGT TTTATTCTGC TCTCCCTTGC
ATCCCACCTT TCTAAGTTGT AAACATAATA GTTGACACA GATTGACAGA TTAAGAAAGG CTTGTGATTG
55 TGCTAGACCT ATGCCTATGC CTCTGTCTCA CCAGATTCCA GGTGTATATG TGGAGGTGGG ATAGGGAGTG
GAGTAAGTGG GTAAATATTA AATTGCCAG TTGGGCACCA TCCTGAATAT TATCTCTAAA GAAAGAAGCA
AAACCAGGCA CAGCTGATGG GTTAACCAGA TATGATACAG AAAACATTTT CTCTGCTTTT TTGGTTTAA
GCCTATATTT GAAGCCTTAG ATCTCTCCAG CACAGTAAGC ACCAGGAGTC CATGAAGAAG ATG GATCTTCATG
TGGAATGACT GGTTCATTC AATAGACTTA ATTCAGCAGT CTGTGGGGAA GAGCAAGGTA TGATAGAATG
60 GTTCCTCAAG TGCTTCAGAT GTGAAGTGGG TTAAATATA CTGTCCCTGT CTCTTCAGA GTTTTGGTAA

AGATAAAATA GGACACTCAT TTAAAAGCAA TCTTTGCAAA TGACAAGCCA CTATAGACAT TAATAGAGTT
TTCATTTCCA GTATTATCAT TAATATCAGA TCCTGGAAGA AGGTTGAGCC TTGACCTAGA GCAAAAAAAC
AGAAGAATTA GTAAAGGAAT CCTGGAGAAA GCCCTGCTG TGTATTTAAA GGAGAAAGGG AGATCATGTT
GGGAAATTAT AATATTAATA GTAAACAAAA GCTAGGAAGT AAAATAAAAAT AAATTATATG GCCTAGATCC
5 CCATAAGTAA TGGTTTAACT TCTGCCTTCC TGTGTTCTGA GCCAGATTAG GGCACAGTAG AGAAAGAGGA
GTCTCTGAAA ATGTTTCCAA TTTCGCTGGT CAGACAGCGG ATCATCAGTG AATCAGATGA AAATTTGTGG
ATTTATGCAC TAACTGATCA GCAGGAAAT AAACAAGAAA AGCGTTGGTA GCTCTGGTGA ATCCCAAAAG
AATTTGGCAG TTGCTAGCCA TGCTCCTGAA TATGTATAAA CAGTACATCA TATGACTAAG AGTTTGACTT
AGGGGTTAGA TTTTATGTGT TTGAACCCCA AATTAGTTAT TTAATAGTTG GCACCCCAAA ACAAGTTACT
10 TAACCTCACT AAGATTCAGT TTTCCTGTTT ATAAAATGTA GATAGTGATA GTATGTACTT TATAGGATTA
TTGTGAAAAA TAAATGAAAT ATCAGATTTA TTTAGGATAA CACCTGGCAT ATGTTTGGTA TTCAGTAATT
AGTTGCTGCT GTTTTATTCT GCTCTCCCTT GCATCCCACT TTTCTAAGTT GTAAACTAAA TAGTTGTACA
CAGATTGACA GATTAAGAAA GGCTTGTGAT TGTGCTAGAC CTATGCCTCT CTCTCACCAG ATTCCAGGTG
TATATGTGGA GGTGGGATAG GGAGTGGAGT AAGTGGGTAA ATATTAAATT GCCCAGTTGG GCACCATCCT
15 GAATATTATC TCTAAAGAAA GAAGCAAAAC CAGGCACAGC TGATGGGTAA ACCAGATATG ATACAGAAAA
CATTTCCCTC TGCTTTTGG TTTTAAGCCT ATATTGAAG CCTTAGATCT CTCCAGCACA GTAAAGCACA
GGAGTCCATG AAGAAGATGG CTCTGCCAT GGAATCCCT ACTCTACTGT GTGTAGCCTT ACTGTTCTTC
GGTAAGTAGA GATTCAATTA CCCCTCCCAG GGAGGCCCAA ATGAATTTGG GGAGCAGCTG GGGTAGGAAC
CTTTACTGTG GGTGGTGA CTCTTAGGA CATGTGCAAA CTATTGGGCA TTTCCCAGGG ACTCTGTAGT
20 GGAGCCAAGC TAGAAAGCAG AGGCAAGTGG GCTGAGCAAC ACCTAAGGAG GAAGCCAGAC TGAAAGCTTG
GTTCTTGCA TTTGCTCTGG CATCTCCAG AGTGCAAAAT TCCTACCAAG GTAATGAGGG TAGAGGAGAG
AAAGAAGCTC TTTCTCCCC TGATTCTCAT TCCTGAAAAG ACGTTGGTCT CTTAAATTC CATGGATGTA
GATCTTATCC CCACACCCAG ATTCTAGTCC TCTGGAGATA AAGAAGACTG CTGGACACTA ATGTATCCTC
TCTGGACTTT TGCAGCTCCA GATGGCGTGT TAGCAGGTGA GTCCTCTGTT CTGTTCCTT TGGTGTATCA
25 ACATGTCTGG GCATTGCTTT CCTCTCATA TTTCTTCGT CCCATCACTT CTGCTTTCTA ATGAGCATGA
ATCTGTTCCT TGGCCAGAT ACTTCCCTC TCCACCTGCT CTTGTCTTTC TTTTTTCCC TATTGATTG
CATTCTCTCA AGTCATTCTC TCCTCTGTTT TAGTCAATAA CCATGTCTGT TGCACATATA CATGTCTCAT
TCTCTCTCCT AGACACTTTG GCATGATCTC GCTCAATAAT TACATTATTA TTATTATTGC CATTTTATAA
TTGAGGATGC TGAAACTCAG TGATTTTCTG GTGGTTACAT GGCTAAGGAA CTGGATTTC ACGTAAGTTC
30 CTTGGATCTA AGTCCAGTTC TCTTCTGACT ATATCACCCT TTTGTTATCA CCATGTATCT ACTTCTTTGG
TCTCTGTTCA AATTTGCACT ACATCCCTT GTTCCAGGAA GCCATTCAAG ACTGACTTTC TTAGTGCCCTC
TCACTACTTT CTGGAACCTGA CATATGTTTT TCACTCTGTA TATACTTACA ATTAATAAGT CATAAATATT
CAGAGCTTGG AGAAACCTTA TATTTTCATCC AGTCCAGTAA ATTTATCCAT CCATAATTCA CTCATTTCATT
CACATAATA ATATTTAATG TAACAATGGT TGAACATGGC AGACAGTGT TCTACCTCAA AAGAGATTGC
35 AGTCTCATT TACAGATACT GAATTGAAAT TAACAGAAGT AGAGTGAGTC AGCTCAAATC ACATAGTGAA
TTGGTTTCTT TGTTTTTAAA TCTCCTGCAT ATGTGTCCTG TCTTCTCCC TGTGTTGGGC GTTCCCTGGG
GCACCAATAC TAATTTCTCC TTCCCTAGA AATCAAAACA GGGTCTTATC ACCAACAGAA TAAGGACAGG
TTGACCACTG ATTGTCAGAA TATTGCTTCG TTTGTACTTT TAAGCCTAGA CAGTTTTCAA TGACTTTTTT
TCTCTCTACA TGTCTTTTCA TATTTTATC TTCTGAAAGT CCCTCAGAAA CCTAAGGTCT CCTTGAACCC
40 TCCATGGAAT AGAATATTTA AAGGAGAGAA TGTGACTCTT ACATGTAATG GGAACAATTT CTTTGAAGTC
AGTTCCACCA AATGGTTCCA CAATGGCAGC CTTTCAGAAG AGACAAATTC AAGTTTGAAT ATTGTGAATG
CCAAATTTGA AGACAGTGGA GAATACAAAT GTCAGCACCA ACAAGTTAAT GAGAGTGAAC CTGTGTACCT
GGAAGTCTTC AGTGGAAGT TCCAGGGATA TGGAAATACA GATCTCTCAT GTGAGGGATG GTCATCTGTA
AGATGGGAAA AAACAGGTTA TTCCAAGGGT TAGGACACCA GAGTGGGATT CAAGGCCTCT CATTTTTAAG
45 ACCCCTGCAT TGGCTGGGCA CAGTGGCTCA CGCCTGTAAT CCCAGCACTT TGGGAGGCTG AGGCAGGTGG
ATCACGAGGT CAGGAGATCG AGACCATCCG GCTAACATGG TGAAACCCCA TCTCTGCTAA AAAATATATA
TATATAAAAT TAGCCGGGCG TAGTGGTGGG CACCTGTAGT CCCAGGTACT CGGGAGGCTG AGGCAGGAGA
ATGGTGTGAA CCCAGGAGGT GGAGGTTGCA GTGAGCTGAG ATCACGCCAC TGCTCTCCAG CCTGGGCTAC
AGAGCAAGAC TCCGTCTCAA AAAATAAATA AATAAATAAA AAAGACCCCT GCATCTCTTT TCTTCTACCC
50 CCTTCCCTTT TGATTACTTG TATGCTTCT TTCAATATTC TAGTCATCTC TCAATATTAT TCCTCCACCC
TATTTTCTCT TATCTTTTCT GCCTAGATTG AGGTATATAT TATGTGGTCA AACAGCATGA CATATATGTG
AACATTTCAA AGAGCTGTGT ATCTGGAATA GGATCAAAAG GTTTGACTTA AAGTTTGTCT CTGCATAATC
CATATGGCAG CACCTGAATA TTAGTTGTA CTCTTCGTTA TGAAACATAT CTGGGTACAT TTCCTTATGT
CCTCTGTGT TACTTAAGAA CACATATTTT ATGCTTGTIT CATTTTATC ACTCCTACTG CCAACAAATA
55 GCATAGCATG CTTAGGCACA TGTGGCTTAA TTAGCAAATG TTGAATAAAC AAATTAATGA TTTTGAATAG
TGACCAATAG GTCTCTTTTA TACTCTATAT TTTTCTCTG AGTGAAAAAA AATGTTTCAA CCTCCATATG
TAAATTCCAA ACACAACTA AAGCAATGTA GAATAGCTTC TTTATCCCT GGAGTAGGTT CTAGAGAAGT
CCTAAAGGAT TGGTCCTAAA TTAATTATGC TTATTATGCT AGCGATATTT CCTTTCAAAA TTCTCTTTA
ATGAATGCTT TTTAATTTT ACAAAAGCAT TAACCATAGA ATGTGATTCT TGTCTTTCAC TGACTCATT
60 GTGACAAATA TTTGTTGAGT ACCTACCAAC TCCTAAGTAT TGCTACCAAC CCTTAAATAT TGTGTTGGGC
ATTCAGAATA GAATGTAGAA CTAGACAGGG TCCCTGACTT CTGGAGCAG AGAGCAGTAT GGAAGAGGA
CATTAAATAA AGAATTACAT AAGTAATTAA TTTAAATTAT ACATGTTTTG AAGAAGTTTT TTTTGTACAA

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CTATAATTAA CACTAGAACT GGGAAAGTTTC TATAAGGTAA GAGAGGACAA AATAGACACT CTCCTAAGCT
 AAAATTCCCA AGAAAGACTG TTTATTTTCC CCTAACTAAC TAGAACTAGC AACAGAAGAT CTGAAAGGAA
 TTCTGGCTTT CAAGTGTTCC ATGTATGGAC TCATCAGGGA GGTCCGAGAG GCTTTGTGGC CCCAGACTGA
 CTTTTCAGGA GGGGAAAGGA TTTATCAATA CACAAGACAG GCTCTAAGCA TTATTTGTG CCCTTTAAAA
 5 ATCCACTTTA TGAGCCAAAA AGTGAGTTAA TGATAATTCA TAGTTTCTGA CACATGCTCT ATGCGTGGCT
 CTCTTTTCTC TATTCATTCT CTCTCTCTC ATTTATTGTT AAATAAATAA TGTAATGAAT GTTCTTCAGA
 CTGGCTGCTC CTTCAGGCCT CTGCTGAGGT GGTGATGGAG GGCCAGCCCC TCTTCCTCAG GTGCCATGGT
 TGGAGGAACT GGGATGTGTA CAAGGTGATC TATTATAAGG ATGGTGAAGC TCTCAAGTAC TGGTATGAGA
 ACCACAACAT CTCCATTACA AATGCCACAG TTGAAGACAG TGGAACCTAC TACTGTACGG GCAAAGTGTG
 10 GCAGCTGGAC TATGAGTCTG AGCCCTCAA CATTACTGTA ATAAAAAGGTG AGTTGGTAAA GGAAAGGAAA
 AGCATCCATA GCAGGGGAAG GAAGAGAGAA CTCTGAGCC TGAGCAGTTG CAGCTTGTAG AAGGGGGGCA
 CCTGTGATAC ACTGGAAAGC CTACCAGACT TGCAATGAGG AGACCTGGGT GATAGTATAT ATCTCAATCT
 CTGTTTCAAA GCCTTGACTT GTTAAATGGT GATAGTAATA CCTGCTTGCA CTATGAAATT TTTATGAAGA
 TTAATGTGGT AATATTTGTG AAATGACTTT GTAAACTGTT AAGCACTACC CAAGCATAAC AGATTGTGAT
 15 TACTATTTTG ATCTCAAAGT CATCTGTTGC TCCTGGGGGA ACACCTATAT TTATCAAATT GAAAAAAGT
 TTCAAAGTTG AATGAAGAAA GGATATAAAG AGCTTGAGGA GCCCATTCCA GCTTAGGAGG GCTGGGAAAG
 GAAACCGACA AGTCAGTAAG CTGTGTGCCT GTGTATTGAG GGAGGAGGGA ATGGACTTGA TATGGAGAGG
 GTAGGGAGGT GGA CTGCTCCTC TATGGCCTGT AAGAAAAAAGT GCTCTCTCCA AACTCTTTAT AAGAGAGGGA
 GCCTGTGAAG TATTCACTTT TGAAGGAGAA AGTTAGACTT TTCCTTCACA CACTTTGTAC ATAATAATGT
 20 TTAaaaaAGC ATGAGGTCAA AATACATAAT TAAGTCTAG CAGTTCTCTG TTAATAATT TGAGACTGAA
 GTGCTATGTA CTGTCTCTA GGCTTCCAGT ATCTTCATCT GTAAAAACAGA ATATTTGGTC TAGATTCCAT
 TAGAATCATT TGATAACTTA AAAAAATATAT TGATGCTCAT GTCTCATTTT TTAGATTCT GATTAAATTG
 GTTTGGGGTG CAGCCTGGGT ATACGTATTT TTCATAGGTC TTCACATAA TGGTAATGGG TAGCCAATAT
 TGAGAATCAC TTGTCTAGGT GATCTTTAAA TGATTTCTGG ATGTAATATT CTGAGGCTCT ATAATTGAG
 25 ACTAATCACA AAAATCGGTA CAGTTTATAA ACAGACTAAC AGAACCACAA AATAATAGAA TTGGAAGGCA
 ATTTAACTAG TGCAATTTCT TCATTTTGCC TAACAGGCAT GTAAGAAATG ATGATTGATT GAGTAATAGG
 CATTGATGAC CCTGTCTCTC ACTTTGTCCC CTTTCCACCC CTTAATTATA TGTGAATTCT GGTCTTGCA
 TTTCGAATAA GGGGTTTATC TTTCTATTG TCTTCCCCTC TGGGCACGGC ACACTGGCTA CTGGAGTTAA
 GAGGAAATGC TTAGGACTCC CTGTGGCTCC AGGGAGCACC AACAGAGCAA CTCAACCTAG TGTTAATCTG
 30 AGTGTTTTCT CTGTGCTTCT GGATGCCACA TCACGCTAAA AATGAAGGAC AAAGCTTGGT CTTTCTCTTA
 GGGAGGATGA AACTCTGAAC CTCATTTTTC AGTTCCCAAG ATGAATTATG TTTCTCATTTG CATCTGTGTT
 CCACTACAGC TCCGCGTGAG AAGTACTGGC TACAATTTTT TATCCCATTG TTGGTGGTGA TTCTGTTTGC
 TGTGGACACA GGATTATTTA TCTCAACTCA GCAGCAGGTC ACATTTCTCT TGAAGATTAA GAGAACCAGG
 AAAGGCTTCA GACTTCTGAA CCCACATCCT AAGCCAAACC CCAAAAACAA CTGATATAAT TACTCAAGAA
 35 ATATTGCAA CATTAGTTT TTCCAGCAT CAGCAATTGC TACTCAATTG TCAAACACAG CTTGCAATAT
 ACATAGAAAC GTCTGTGCTC AAGGATTTAT AGAAATGCTT CATTAAACTG AGTGAAACTG GTTAAAGTGGC
 ATGTAATAGT AAGTGCTCAA TTAACATTGG TTGAATAAAT GAGAGAATGA ATAGATTCTT TTATTAGCAT
 TTGTAAGAAG GATGTTCAAT TTCAATAAAA TAAATATAAA ACCATGTAAC AGAATGCTTC TGAGTATTCA
 AGGCTTGCTA GTTTGTTTGT TTGTTTCTA CTAAAGGCAA GGACCATGAA GTTCTAGATT GGAATGTCC
 40 TCTCTTGACT ATTGCAAGTG CGATCTAGGA ATGAAAAGAC ATAGGAGGAT GCCAGTGAGG TGGATCATT
 TTATGCTTCT TCTTCAGCTT ACTAAATATG AACTTTTCAGT TCTTGGCAGA ATCAGGGACA GTCTCAAGAC
 ATAGGACTCT CAGGATGAAG TAGAGTCCAG GATTCCTCTG TGATTGTTTT GCCCTCCCA AATTTATATC
 TTGAACCTAT GTCTTGATC TTTATACAGC ACCTGAACCA AGCATTTTGG AGAAATTCCA GCTAATAATA
 ATAACCAAAA CCTTCGGCTC TGAAAAACAGT CCAGACTGTA ATAAGATCTT GGGCAAAAAGA ACTGACAGT
 45 TTTGGTTTAT TTTCCCTTTC ATTTTATGTC TTCATCATAG TCATTGGAGG CTCATTCTTC TTGTCATGGA
 GTAAATGGGA TTAAAGTTC TACTAAGAGT CTCCAGCATC CTCCACCTGT CTACCACCGA GCATGGGCCT
 ATATTGAAG CCTTAGATCT CTCCAGCACA GTAAGCACC AAGAGATGG CTCCTGCCAT
 GGAATCCCCT ACTCTACTGT GTGTAGCCTT ACTGTTCTTC GCTCCAGATG GCGTGTTAGC AGTCCCTCAG
 AAACCTAAGG TCTCCTTGAA CCCTCCATGG AATAGAATAT TTAAAGGAGA GAATGTGACT CTTACATGTA
 50 ATGGGAACAA TTTCTTTGAA GTCAGTTCCA CCAAATGGTT CCACAATGGC AGCCTTTCAG AAGAGACAAA
 TTCAAGTTTG AATATTGTGA ATGCCAAATT TGAAGACAGT GGAGAATACA AATGTCAGCA CCAACAAGTT
 AATGAGAGTG AACCTGTGTA CCTGGAAGTC TCTAGTACT GCGTGCTCT TCAGGCTCT GCTGAGGTGG
 TGATGGAGGG CCAGCCCCTC TTCTCAGGT GCCATGGTTG GAGGAAGTGG GATGTGTACA AGGTGATCTA
 TTATAAGGAT GGTGAAGCTC TCAAGTACTG GTATGAGAAC CACAACATCT CCATTACAAA TGCCACAGTT
 55 GAAGACAGTG GAACCTACTA CTGTACGGGC AAAGTGTGGC AGCTGGACTA TGAGTCTGAG CCCCTCAACA
 TTAAGTGAAT AAAAGCTCCG CGTGAGAAGT ACTGGCTACA ATTTTTTATC CCATTGTTGG TGGTGATTCT
 GTTTGCTGTG GACACAGGAT TATTTATCTC AACTCAGCAG CAGGTCACAT TTCTCTTGAA GATTAAGAGA
 ACCAGGAAAG GCTTCAGACT TCTGAACCCA CATCCTAAGC CAAACCCCAA AAACAACCTGA TATAATTACT
 CAAGAAATAT TTGCAACATT AGTTTTTTTC CAGCATCAGC AATTGCTACT CAATTGTCAA ACACAGCTTG
 60 CAATATACAT AGAAACGTCT GTGCTCAAGG ATTTATAGAA ATGCTTCATT AAAGTGAAGT AAAGTGAAGT
 AGTGGCATGT AATAGTAAGT GCTCAATTAA CATTGGTTGA ATAAATGAGA GAATGAATAG ATTCAATTAT
 TAGCATTTGT AAAAGAGATG TTCAATTTCA ATAAATAAAA TATAAACCA TGTAACAGAA TGCTTCTGAG

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 ATAAAAAGGG TCGGGCGCGG AGGCTCACGC CTGTAATCCC AGCCCTTTGG GAGGCCGAGG TGGGCAGATC
 ACGAAGTCAG TAGTTTGAGA CCAGCCTGGC CAACATAGTG AAACCCCGTC TCTACTAAAA ATACAAAAAA
 20 AAAATTAGCT GGGTGTGGTG GCAGTCACCT GTAGTCCAG CTACTTGGGA GGTATGAGGA GGAGAATCGC
 TTGAACCTGG GAGGCCGAGG TTGCAGTGAG CCGAGATCGC ACCAGTGCAC TCCAGCCTTG GTGACAATGG
 GAGACTCCAT CTCAAAAAAA AAAAAAAGATA AAAAGTCAGA AATCTGAAAA GTGGAGGAAG
 AGTACAAATA GACCTAAATT AAGTCTCATT TTTTGGCTTT GATTTTGGGG AGACAAAGGG AAATGCAGCC
 ATAGAGGGCC TGATGACATC CAATACATGA GTTCTGGTAA AGATAAAATT TGATACACGG TTTGGTGTCA
 25 TTATAAGAGA AATCATTATT AAATGAAGCA AGTTAACACT CTAAGAGAAT TATTTTGAGA TAGAAGTGAA
 GCTAAGCTAA ACTTCACATG CCTATAATTG GAGGGAAAAA CTAAGGATAA AATCTAGCCT AGAAGATACA
 ATAATTAGTC ATAAACATGC ATTGTGAAAC TGTAGAGAGC AGGTAGCCCA AAATAGAGAA AGATTAGATA
 AAGAGAAAAAT AAGTATCCAT CAGAGACAGT ATCTTAGGC TGGGCAAGA TGAATGCAAA AGGTGCTGAG
 CAACTCCACC TAAGGCATGA ATATGCGGCA GAGAAAAACAG CAATAGTGAA TGAATGCAAA AGGTGCTGAG
 30 CAAATTCCAC ACATGAGTAT TGTGCATGAG TAAATGAATA AAACATTTGC AAAGACCTTT AGAGAAAGAG
 AATGGGAGCA TATGTGCGAA ATAAGATAGT TGATTATGAA TAGAAGGTAG TGAAGAAAAG CAAGCTAAGA
 AAAAATTCTG TTTATAAAAG AAGGAAAAGA TAGTTTATGT TTTTAGCCTA AGTATAAGAG TCCTACAGAT
 GGACTGAAAA AAATCAGTCT GAGAGTATTA GTCACAATTA ATGAAATAAT TACATTTTAT GTATTGAGGA
 TGCCAAGATT AAAAGGTGAC AGGTAGATGT TAATTTCCCT AGATTGTGAA AGTGATCACG ACAATCACAC
 35 AACAAATAAT TAAGTGAATT GGTATGCTTT ATTTAATTGT AGGGCCTGAG GTTTTCCATT CTCATTTTTC
 TAAAAATACAA TTTTGTCTT CCAAATTGA CAGCAGAATA AAAACCCTAC CCTTTCAGT TGTATCATGC
 TAAGCTGCAT CTCTACTCTT GATCATCTGT AGGTATTAAT CACATCACTT CCATGGCATG GATGTTTACA
 TACAGACTCT TAACCCTGGT TTACCAGGAC CTCTAGGAGT GGATCCAATC TATATCTTTA CAGTTGTATA
 GTATATGATA TCTCTTTTAT TTCACTCAAT TTATATTTTC ATCATTGACT ACATATTTCT TATACACAAC
 40 ACACAATTTA TGAATTTTTT CTCAAGATCA TTCTGAGAGT TGCCCCACCC TACCTGCCTT TTATAGTACG
 CCCACCTCAG GCAGACACAG AGCACAATGC TGGGGTTCTC TTCACACTAT CACTGCCCCA AATTGTCTTT
 CTAAATTTCA ACTTCAATGT CATCTTCTCC ATGAAGACCA CTGAATGAAC ACCTTTTCAT CCAGCCTTAA
 TTTCTTGCTC CATAACTACT CTATCCACG ATGCAGTATT GTATCATTA TATTAGTGT GCTTGTGACC
 TCCTTATGTA TTCTCAATTA CCTGTATTTG TGCAATAAAT TGAATAAATG TAACTTGATT TCTTATCTGT
 45 GTTTGTGTG GCATGCAAGA TTTAGGTACT TATCAAGATA ATGGGGAATT AAGGCATCAA TAAATGATG
 CCAAAGACCA AGAGCAGTTT CTGAAGTCCT CCTTTTCATC AGCTCTTTAT CAAACAGAAC ACTTATAAA
 CAACCCATAG CCAGAAAACA GGATGTAGGA ACAATCACCA GCACACTCTA TAAACAACCC ATAGCAGAA
 AACAGAATGT AAGGACAATC ACCAGCCATC TTTTGTCAAT AATTGATGGA ATAGAGTTGA AAGGAACTGG
 AGCATGAGTC ATATTTGACC AGTCAGTCCT CACTCTTATT TACTTGCTAT GTAACTTGA GAAAGCTTTT
 50 TTCTCTTTGT GAACCTCAGG TTTTACATCT GAAAATGAGA AATTGGAAC AAAAGATTCC TAACTGGTCT
 TTCTGTTCCC ATATTCTGTG ATTTTCAAT ATTTAGGATT TTTGGTAATC TTTCAAAGGA GTAGCTCTCC ACTTTGGGTA
 TGAGATAGCA ACACGAATCA GAACTATTTG GTGGACATAT TTTCAAAGGA GTAGCTCTCC ACTTTGGGTA
 AAGAAGTGAT CGNGGTCGTG GTGGCTCAGC CCTGTAATCC CAGCACTTTA GGGAGGCCAA GGCGGGTGGA
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 55 AAATTAGCCA GGCGTGGTGG CGGGCGCCTG TAGTCCCACG TACTCGGGAG GCTGAGGCAG GAGAATGGCA
 TGAACCAGGG AGGCGGAGCT TGCCGTGAGC CGAGATAGCG CCACTGCAGT CCCTCCTGGG CAAAAGAGCA
 AGACTGCGTC TCAAAAAAAA AAAAAAAGAA AAAAAAGAA GTGTGTGGAG TAGCAGGACA CCTGCAACAA
 TAATATTTT CTAAATCCCT CTGAAAAATG CTAATCAAAG GGTTTTTTTC CTAAAAATTG TCTTAGAAAT
 60 AAAATTTCCC CTTTGGGAGA CCGAGGCTGG CAGATCACGA GGTGAGGAGA TAGAGACCAC GGTGAAACCC
 CGTCTCTACT AAAAATACTA AAAATTAGCT GGGNGTGGT GGTGGGTACA CCTGTAGTCC CAGCTACTTG
 GAGGCTGAGG CTGGAGAATC ACGTGAAC-3' (FRAG. NO:) (SEQ. ID NO:2504)

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Human Histidine Decarboxylase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT CCC TTG GGC TCT GGC TCC TTC TC TCT CTC TCC CTC TCT CTC TGT CGC CTC CGC CCT GGC TGC
TGG GGT GGT GGT GC TTT TGT TCT TCC TTG CTG CC GCC CCG CTG CTT GTC T TC CTC G CTC TGT CCC TCT
CTC TCT GTB CTC CTC BGG CTC CBT CBT CTC CCT TGG GC-3' (FRAG. NO:1700) (SEQ. ID NO:1711)

5 5'-GGC TCT GGC (FRAG. NO:1701) (SEQ. ID NO: 1712)

5'-CCC TTG G (FRAG. NO:1702) (SEQ. ID NO: 1713)

5'- TT TGT TCT TCC (FRAG. NO:1703) (SEQ. ID NO: 1714)

5'- TCT CCC TTG GGC TCT GGC TCC TTC TC-3' (FRAG. NO:1024) (SEQ. ID NO: 1034)

5'- TCT CTC TCC CTC TCT CTC TGT -3' (FRAG. NO:1025) (SEQ. ID NO:1035)

10 5'- CGC CTC CGC CCT GGC TGC TGG GGT GGT GC-3' (FRAG. NO:1026) (SEQ. ID NO:1036)

5'- TTT TGT TCT TCC TTG CTG CC-3' (FRAG. NO:1027) (SEQ. ID NO:1037)

5'- GCC CCG CTG CTT GTC T TC CTC G-3' (FRAG. NO:1028) (SEQ. ID NO:1038)

5'-CTC TGT CCC TCT CTC TCT GTB CTC CTC BGG CTC CBT CBT CTC CCT TGG GC (FRAG.NO:1029)(SEQ.ID NO:1039)

Human Beta Tryptase Nucleic Acid and Antisense Oligonucleotide Fragments

15 5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CCG GGT GTT CCC GGC GGG CCT GGC CTG GGG CBG GGG CCG
CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GBT TCB GCB TCC TGG-3' (FRAG.
NO:1704) (SEQ. ID NO: 1715)

5'- GCT CCT GGG GGC CT-3' (FRAG. NO:1705) (SEQ. ID NO: 1716)

5'-CGT BGG CGC-3' (FRAG. NO:1706) (SEQ. ID NO: 1717)

20 5'-T GGC CTG GGG-3' (FRAG. NO:1707) (SEQ. ID NO: 1718)

5'-CTT GCT CCT GGG GGC CTC CTG-3' (FRAG. NO:1030) (SEQ. ID NO:1040)

5'-GTC CCT CCG GGT GTT CCC GGC-3' (FRAG. NO:1031) (SEQ. ID NO:1041)

5'-GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB
GBT TCB GCB TCC TGG-3' (FRAG. NO:1032) (SEQ. ID NO:1042)

Human Tryptase-I Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CTG GCT G TT CCC GGC CCT GGB CTG GGG CBG GGG CCG CGT
BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GGC TCB GCB TCC TGG CCB CGG BBT TCC-3'
(FRAG. NO: 1708) (SEQ. ID NO:1719)

5'-CT CCT GGG GGC CTC CTG-3' (FRAG. NO:1709) (SEQ. ID NO:1720)

30 5'-B TCC TGG CCB CGG BBT TCC -3' (FRAG. NO:1710) (SEQ. ID NO:1721)

5'-GTC CCT C-3' (FRAG. NO:1711) (SEQ. ID NO:1722)

5'-CTT GCT CCT GGG GGC CTC CTG-3' (FRAG. NO:1033) (SEQ. ID NO:1043)

5'-GTC CCT CTG GCT G TT CCC GGC-3' (FRAG. NO:1034) (SEQ. ID NO:1044)

Human Eosinophil Cationic Protein Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCT CCT TCC TGG TCT GTC TGC CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC CBG TCT CTG BGC TGT GGC-3' (FRAG. NO: 1719) (SEQ. ID NO: 1732)

5'-TTC TCC TTT GGT T-3' (FRAG. NO:1720) (SEQ. ID NO: 1733)

5 -5'-T TTC TCC TTT GGT T-3' (FRAG. NO:1721) (SEQ. ID NO:1734)

5'- GGG CGC GGG CGB GCB TCG C-3' (FRAG. NO:1042) (SEQ. ID NO:1052)

5'- TTT GGG CTT TTC TCC TTT GGT T-3' (FRAG. NO:1043) (SEQ. ID NO:1053)

5'-TGB GCG CCB GGB CCG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3' (FRAG. NO:1044) (SEQ. ID NO:1054)

Human Eosinophil Derived Neurotoxin Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC CTG CTG CTC TTT CTG CT TCC CTT GGT GGG TTG GGC C GCT GGT TGT TCT GGG GTT C TTG CTG CCC CTT CTG TCC C TGT TTG CTG GTG TCT GCG C 5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3' (FRAG. NO: 1722) (SEQ. ID NO: 1735)

5'-TTC CTG T-3' (FRAG. NO:1723) (SEQ. ID NO: 1736)

15 5'-CTC TTT CTG CT-3' (FRAG. NO: 1724) (SEQ. ID NO:1737)

5'-CCC CTT CTG TCC C-3' (FRAG. NO:1725) (SEQ. ID NO: 1738)

5'- GCC CTG CTG CTC TTT CTG CT-3' (FRAG. NO:1047) (SEQ. ID NO:1055)

5'- TCC CTT GGT TTG GGC C-3' (FRAG. NO:1048) (SEQ. ID NO:1056)

5'- GCT GGT TGT TCT GGG GTT C-3' (FRAG. NO:1049) (SEQ. ID NO:1058)

20 5'- TTG CTG CCC CTT CTG TCC C-3' (FRAG. NO:1050) (SEQ. ID NO:1057)

5'- TGT TTG CTG GTG TCT GCG C -3' (FRAG. NO:1051) (SEQ. ID NO:1059)

5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3' (FRAG. NO:1052) (SEQ. ID NO:1060)

Human Eosinophil Peroxidase Nucleic Acid and Antisense Oligonucleotide Fragments

25 5'-GCG CTC GGC CTG GTC CCG G GGG TCT CCT CTT GTT GTT GC TTG CGC CTC CTG CTG GGG GT CC CTC TGT TCT TGT TTT GGG GGC GGG CCC GGC CGT TGT CTT G GTT TGG GGG TTT CCG TTG GGG TTC TCC TGG CCC GGG CCT TGC CC GGC CGT GGT CCC GGC TTC GTTCCT CTC TCC GTC TCG GCT CTT CTG GGG CCT TGC GCT GTC TTT GGT G 5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC CACCGCTCCT GTCAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG

30 GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC CAGGCTGGTA GGAGGTGGGG TGGGGGGTTT CAGTCTCAAA ACTCCCATGA AAACAGAGA GAAGTTTCAG AACTCCACCC AAGAGGCTGG GTTCTAGGG CCCAGAGCTG CCCTCCCCCA CCCTAGAATG GGCTATAAAA GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG AGGGGAGCAG AGGATCCTCC CGTGACAGGT GTGGATGTCA CTCACTTCCC AGCTGGTGAA GCCTCGCTGC

35 AGAGATGCAT CTGCTCCCAG CCCTGGCAGG GGTCTGGCC ACACTCGTCC TCGCCAGGCC CTGTGAGGGC ACTGACCCAG GTAATAGTCC CTTAGACAGG CAAGGAGGAG GGAGGGGAAA TGAAGGGGA AGCACTTGGG TCTTGGAGGG GGTCTGTGTC CTTGCTGAAC CCTGAGTCCC CATCTCTTG AACAGCCTCC CCTGGGGCAG TGGAGACCTC GGTCTGCGA GACTGCATAG CAGAGGCCAA GTTGCTGGTG GATGCTGCCT ACAATTGGAC CCAGAAGAGG TGGACTTGGG TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT TAATACCTTG TGGGTCAGG

40 GAGCCCATGT CCCGTGCTGA TGTTATTTCC CCACCAGGTC CGGGCTGTCT CCAACCAGAT TGTGCGCTTC CCAATGAGA GACTGACCTC CGACCGTGCC CGAGCCCTCA TGTTTCATGCA GTGGGGCCAG TTCAATGACC ATGACCTGGA CTTCTCCCCG GAGTCCCCGG CCAGAGTGGC CTTCACTGCA GGC GTTGACT GTGAGAGGAC CTGCGCCCCAG CTGCCCCCCT GCTTCCCAT CAAGGTACCT ACCCTCAGCC AATCTCCCAT GCCCTGTGT GGCCTCCCC AAAGGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT AAGGAGCTGC

45 CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG CACTGTCTCC TCTTCCATCT CAGATCCCAC CCAATGACCC CCGCATCAAG AACCAGCGTG ACTGCATCCC TTTCTTCCGC TCGGCACCCT CATGCCCCCA AAACAAGAAC AGAGTCCGCA ACCAGATCAA CGCGCTCACC TCCTTTGTGG ACGCCAGCAT GGTGTATGGC AGTGAGGTCT CCTCTCGCT CCGGCTCCGC AACCAGACCA ACTACCTGGG GCTGTGGCC ATCAACCAGC GCTTTCAAGA CAACGGCCGG GCCCTGCTGC CCTTCGACAA CTTGCACGAT GACCCCTGTC TCCTCACCAA CCGCTCGGCG

50 CGCATCCCCT GCTTCTGGC AGGTCAGACA GGGAGGAAGG TGGTGTCTTC CCAGGAACA GGCATCCCTG GGGTCCCAAC TGGGAAGCAA TGGTGGGATG TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC AC TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGGCCC ACCCGTCTC TCCCATCCCC AGCCCTGGGT CTACCCTGGT AGAAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG CTTGGGGTTT TCAAGGTGAC ACCCGATCAA CGGAAACCC CAAACTGGCA GCCATGCACA CCCTCTTTAT

55 GCGAGAGCAC AACCAGCTGG CCACCGAGCT GAGACGCCTG AATCCCCGGT GGAATGGAGA CAAACTGTAC AATGAGGCTC GGAAGATCAT GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCCAGCAT CCCCC CTTTGTATCT CCACCCACCA ATAGTAAATT AATGTTGTCA CATTGACGT GATGACAATA AAGAATATGT CTGAGCCACC CTTTGAAGAG GCAAGGGTAT GGGTGAGTAG CCTCTGGGA ATGTTCTCTC TGTTCTCCCT TCCAGATCAT CACCTACCGA GACTTCTG CCTTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCTGGG GCACTACAGG

60 GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCTGGC CTTCCGCTT GGCCACACAA

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TGCTCCAGCC CTTCATGTTT CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCACT
 TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGTGACCAGG TTTTCCAGGG GGCAAATGGG
 GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTTCCTGAC
 5 AAACGTTACT AACATACCCG ACTGGCTTGT CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCCAAAGT
 AGCTTCCAG AGGCTGGTCC AATCTGTGCT GCTCACATTC CCTGCCACCA GGGGGCATCG ACCCCATCCT
 CCGGGGCCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC
 CGGCTGTTTC GGCAAGTGAG GAGGATTGGT CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC
 ACGGCCTTCC AGGTGAGGGG GCTGTCCACC TCTTCTCCCA GCTTTGCTCG GGCCAGGCTG CTCAAGGGGT
 TCTGGGAAGA CCCTGGTACC CGACTGCCTG GTAGGTCTTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAG
 10 ACAGCGCAAG GCCCTGAGCA GAATTTCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT
 TCAAGGGACA TCTTCAGAGC CAACATCTAC CCTCGGGGCT TTGTGAACTG CAGCCGTATC CCCAGGTTGA
 ACCTATCAGC CTGGCGAGGG ACATGAGGCT TCTGCAGGTA AGGGGAGGCC ACCTCCAGCA CCCTGGGCTG
 GTTAAGCCTC ACATCCTTCC CTGGATGGAT GGCTGAGTCC TCTTAGGTCT CTAAGCAGAG AAAACAGAAC
 TTGTCACTAG GTACTCTTTC CAAGTGGCTT CCCAATGTGC TAGTTTCTGG GCTGACAGTC AATTCCAGGC
 15 CCTAGGACTT TGGGGGAAA TTAGGAGCAT CCAACTA GAATTCCTG GCCAGGACCC CTGCCAGGGC
 ACTGACCCAG CCTCCCCTGG GGCAGTGGAG ACCTCGGTCC TGCAGACTG CATAGCAGAG GCCAAGTTGC
 TGGTGGATGC TGCCTACAAT TGGACCCAGA AGAGCATCAA GCAGCGGCTT CGCAGCGGTT CAGCCAGCCC
 CATGGACCTC CTGTCTACT TCAAACAACC GGTAGCAGCC ACCAGGACAG TTGTTCCGGC CGCAGATTAT
 20 ATGCATGTGG CTTTGGGGCT GCTTGAAGAG AAGTTACAAC CCCAGCGGTC CGGACCCTTC ATTGTCACTG
 ATGTGCTAAC AGAACCACAG CTGCGGCTGC TGTCCAGGC CAGTGGCTGT GCTCTCCGGG ACCAGGCCGA
 GCGCTGCAGC GACAAGTACC GCACCATCAC TGGACGGTGC AACAACAAGA GGAGACCCTT GCTAGGGGCC
 TCCAACCAGG CTCTGGCTCG CTGGCTGCCC GCCGAGTATG AGGATGGGCT GTCGCTCCCC TTCGGCTGGA
 CCCCAGCAG GAGGCGCAAT GGCTTCCTTC TCCCTCTTGT CCGGGCTGTC TCCAACCAGA TTGTGCGCTT
 CCCCATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC ATGTTTCATGC ATGTGGGCGCA GTTCATTGAC
 25 CATGACCTGG ACTTCTCCCC GGAGTCCCCG GCCAGATGG CCTTCACTGC AGGCGTTGAC TGTAGAGGA
 CCTGCGCCCA GCTGCCCCCC TGCTTTCCCA TCAAGATCCC ACCCAATGAC CCCCGCATCA AGAACCAGCG
 TGA CTGCTCATC CCTTTCTTCC GCTCGGCACC CTCATGCCCC CAAAACAAGA ACAGAGTCCG CAACCAGATC
 AACGCGCTCA CCTCCTTTGT GGACGCCAGC ATGGTGTATG GCAGTGAGGT CTCCCTCTCG CTGCGGCTCC
 GCAACCGGAC CAACTACCTG GGGCTGTGG CCATCAACCA GCGCTTCAA GACAACGGCC GGGCCCTGCT
 30 GCCCTTCGAC AACCTGCACG ATGACCCCTG TCTCTCACC AACCGCTCGG CGCGCATCCC CTGCTTCTG
 GCAGGTGACA CCCGATCAAC GGAAACCCCC AAACCTGGCAG CCATGCACAC CCTCTTTATG CGAGAGCACA
 ACCGGCTGGC CACCGAGCTG AGACGCTGA ATCCCGGTG GAATGGAGAC AAAGTGTACA ATGAGGCTCG
 GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA GACTTTCTGC CCTTGGTTCT GGGCAAGGCC
 CCGGCCAGGA GAACCTGGG GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT
 35 TCACCCTGGC CTTCCGCTTT GGCCACACAA TGCTCCAGCC CTTTCATGTT CGCTTGGACA GTCAGTACCG
 GGCCTCCGCA CCCAACTCGC ATGTCCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGTATGAA
 GGGGGCATCG ACCCATCCT CCGGGGCCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT
 TAGTGGATGA GCTCCGGGAC CCGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA
 CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGGTACAAT GCTTGGAGGC GCTTCTGTGG GCTCTCCCAG
 40 CCCCAGGAAT TGGCACAGCT TAGCCGGGTG CTGAAAAACC AGGACTTGGC AAGGAAGTTC CTGAATTTGT
 ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT CGCTGAGCCT CTTTGGCCG GGGCTCGAGT
 GGGGCTCTT TGCGCTTGT TGTTCGAGAA CCAGTTCAGA AGAGCCGAGA CCGGACAGAG TTCTGTGGG
 AGAACGAGGT GTTTTACCA AAGACAGCGC AAGGCCCTGA GCAGAATTTT CTTGTCTCGA ATTATATGTG
 ACAATACCGG TATACCACG GTTTCAAGGG ACATCTTCAG AGCCAACATC TACCCTCGGG GCTTTGTGAA
 45 CTGCAGCCGT ATCCCCAGGT TGAACCTATC AGCCTGGCGA GGGACATGAG GCTTCTGCAG GAGTCTATCC
 CAAGTCTCCA ACTTTTGGAG ACAAGGGGAA GGGGAGGACC ATGAGGCTGC CTTGTCTCCC TGGAGCAAGT
 GCAGGCTCGT GACGCTTCTG CTGGCTACAG CTCAGAGCTG GGTTCCCAG CCAGGAGTGA AGGCTGGGGG
 CTCCTATCAG CAATGGACCT TCCGCCCTTG GAGCCTCTTA GGTATTAGGC TATGAATCAG CGCCACGTGC
 AAAGGCTTGG GAGCCAAGCC ATGTGGTCTT GCACCCAGG CAAGAAAAGT CAGCTGGAGG GTTTACAGCA
 50 CTTTCTACTG TTTCCAGCC CTCCTCCCC TCCCTACCA TGAATAAGAG ACCACTCGGT CCTAGCCTCC
 AGACACCCCA CAATACTCCT CTGAGCCTGA GGCCAGGCAG CATGCTCTGC TTCTACCAAT AAAGCACTGC
 CGGAATTC-3' (FRAG. NO: 1726) (SEQ. ID NO: 3008)
 5'-CACCGCTCCT GTCAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG
 GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC
 55 CAGGCTGGTA GGAGGTGGGG TGGGGGGTIT CAGTCTCAA ACTCCCATGA AAACCAGAGA GAAGTTTCAG
 AACTCCACCC AAGAGGCTGG GTTTCTAGGG CCCAGAGCTG CCCTCCCCCA CCTAGAATG GGCTATAAAA
 GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG
 AGGGAGCAG AGGATCCTCC CGTGCAGGCT GTGGATGTCA CTCACTTCCC AGCTGGTGA GCCTCGCTGC
 AGAGATGCAT CTGCTCCAG CCCTGGCAGG GGTCTGGCC ACACTCGTCC TCGCCAGACC CTGTGAGGGC
 60 ACTGACCCAG GTAATAGTCC CCTAGACAGG CAAGGAGGAG GGAGGGGAAA TGAAGGGGA AGCACTTGGG
 TCTTGGAGGG GGTCTTGTGG CTTGTGAAC CCTGAGTCCC CATCTCTTTG AACAGCCTCC CTTGGGGCAG
 TGGAGACCTC GGTCTGCGA GACTGCATAG CAGAGGCCAA GTTGCTGGTG GATGCTGCCT ACAATTGGAC

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CCAGAAGAGG TGGACTTGGG TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT-3' (FRAG. NO:)(SEQ. ID NO:2483)

5'-TAATACCTTG TGGGGTCAGG GAGCCCATGT CCCGTGCTGA TGTTATTTCC CCACCAGGTC CGGGCTGTCT
CCAACCAGAT TGTGCGCTTC CCCAATGAGA GACTGACCTC CGACCGTGGC CGAGCCCTCA TGTTTCATGCA
5 GTGGGGCCAG TTCATTGACC ATGACCTGGA CTCTCCCCG GAGTCCCCG CCAGAGTGGC CTTCACTGCA
GGCGTTGACT GTGAGAGGAC CTGCGCCCAG CTGCCCCCT GCTTTCCCAT CAAGGTACCT ACCCTCAGCC
AATCTCCCAT GCCCTTGTGT GGCCTCCCC AAAGGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG
CACCATCCTT AAGGAGCTGC CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG-3' (FRAG.NO:)(SEQ.ID NO:2484)

10 5'-CACTGTCTCC TCTTCCATCT CAGATCCCAC CCAATGACCC CCGCATCAAG AACCAGCGTG ACTGCATCCC
TTTCTTCCGC TCGGCACCCT CATGCCCCCA AAACAAGAAC AGAGTCCGCA ACCAGATCAA CGCGCTCACC
TCCTTTGTGG ACGCCAGCAT GGTGTATGGC AGTGAGGTCT CCCTCTCGCT GCGGCTCCGC AACCAGGACCA
ACTACCTGGG GCTGCTGGCC ATCAACCAGC GCTTTCAAGA CAACGCGCCG GCCCTGCTGC CTTTCGACAA
CCTGCACGAT GACCCCTGTC TCCTCACCAA CCGCTCGGCG CGCATCCCCT GCTTCCTGGC AGGTACAGACA
15 GGGAGGAAGG TGGTGTCTTC CCAGGAAACA GCCATCCCTG GGGTCCCAAC TGGGAAGCAA TGGTGGGATG
TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC AC-3'
(FRAG.NO:)(SEQ.ID NO:2485)

20 5'-TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTTGGCCC ACCCGTCTC TCCCATCCCC AGCCCTGGGT
CTACCTGGT AGAAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG CTGGGGTTT TCAAGGTGAC
ACCCGATCAA CGGAAACCCC CAACTGGCA GCCATGCACA CCCTCTTTAT GCGAGAGCAC AACCAGCTGG
CCACCGAGCT GAGACGCTG AATCCCCGGT GGAATGGAGA CAACTGTAC AATGAGGCTC GGAAGATCAT
GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCAGCAT CCCC-3' (FRAG.NO:)(SEQ.IDNO:2486)

25 5'-CTTTGTATCT CCACCCACCA ATAGTAAAT AATGTTGTCA CATTTGACGT GATGACAATA AAGAATATGT
CTGAGCCACC CTTTGAAGG GCAAGGGTAT GGGTGAGTAG CCTCTGGGGA ATGTTCTCTC TGTCTTCCCT
TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCTGGG
GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCTGGC CTTCCGCTTT
GGCCACACAA TGCTCCAGCC CTTCATGTC CGTTGGACA GTCAGTACCG GGCTCCGCA CCAACTCGC
ATGTCCCACT TAGCTCTGCC TTCTTTGCCA GCTGGCGGAT CGTGATGAA GGTGACCAGG TTTTCCAGGG
GGCAAATGGG GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG-3' (FRAG.NO:)(SEQ.ID NO:2487)

30 5'-TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTTCCTGAC AAACGTTACT AACATACCCG ACTGGCTTGT
CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCAAGT AGCTTCCCAG AGGCTGGTCC AATCTGTGCT
GCTCACATTC CTTGCCACCA GGGGGCATCG ACCCATCCT CCGGGGCCCTC ATGGCCACCC CTGCCAAGCT
GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTT GGAAGTGAG GAGGATTGGG
CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGTGAGGGG GCTGTCCACC
35 TCTTCTCCA GCTTGTCTG GGCCAGGCTG CTAAGGGGT TCTGGGAAGA CCCTGGTACC-3' (FRAG.NO:)(SEQ.ID NO:2488)

5'-CGACTGCCTG GTAGGTCTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAAG ACAGCGCAAG GCCCTGAGCA
GAATTTCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT TCAAGGGACA TCTTCAGAGC
CAACATCTAC CCTCGGGGCT TTGTAACTG CAGCCGTATC CCCAGGTTGA ACCTATCAGC CTGGCGAGGG
40 ACATGAGGCT TCTGCAGGTA AGGGGAGGCC ACCTCCAGCA CCTGGGCTG GTTAAGCCTC ACATCCTTCC
CTGGATGGAT GGCTGAGTCC TCTTAGGTCT CTAAGCAGAG AAAACAGAAC TGTCACTAG GTACTCTTTC
CAAGTGGCTT CCAATGTGC TAGTTTCTGG GCTGACAGTC AATTCCAGGC CCTAGGACTT TGGGGGGAAA
TTAGGAGCAT CCAACTA-3' (FRAG.NO:)(SEQ.ID NO:2489)

45 5'-GAATTCCTG GCCAGGACCC CTGCCAGGGC ACTGACCCAG CCTCCCCTGG GGCAGTGGAG ACCTCGGTCC
TGCGAGACTG CATAGCAGAG GCCAAGTTGC TGGTGGATGC TGCCTACAAT TGGACCCAGA AGAGCATCAA
GCAGCGGCTT CGCAGCGGTT CAGCCAGCCC CATGGACCTC CTGTCTACT TCAAACAACC GGTAGCAGCC
ACCAGGACAG TTGTTCCGGC CGCAGATTAT ATGCATGTGG CTTTGGGGCT GCTTGAAGAG AAGTTACAAC
CCCAGCGGTC CGGACCCTTC ATTGTCACTG ATGTGCTAAC AGAACCACAG CTGCGGCTGC TGTCCCAGGC
CAGTGGCTGT GCTCTCCGG ACCAGGCCGA GCGCTGCAG GACAAGTACC GCACCATCAC TGGACGGTGC
50 AACAACAAGA GGAGACCCTT GCTAGGGGCC TCCAACCAGG CTCTGGCTCG CTGGCTGCCC GCCGAGTATG
AGGATGGGCT GTCGCTCCCC TTCGGCTGGA CCCCCAGAG GAGGCGCAAT GGCTTCCTTC TCCCTCTTGT
CCGGGCTGTC TCCAACCAGA TTGTGCGCTT CCCCATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC
ATGTTTCATGC AGTGGGGCCA GTTCATTGAC CATGACCTGG ACTTCTCCCC GAGTCCCCG GCCAGAGTGG
CCTTCACTGC AGGCGTTGAC TGTGAGAGGA CCTGCGCCCA GCTGCCCCC TGCTTTCCCA TCAAGATCCC
55 ACCCAATGAC CCCCGCATCA AGAACCAGCG TGAATGCATC CCTTCTTTC GCTCGGCACC CTCATGCCCC
CAAAACAAGA ACAGAGTCCG CAACCAGATC AACGCGCTCA CCTCTTTGT GGACGCCAGC ATGGTGTATG
GCAGTGAGGT CTCCCTCTCG CTGCGGCTCC GCAACCGGAC CAACTACCTG GGGCTGCTGG CCATCAACCA
GCGCTTTCAA GACAACGGCC GGGCCCTGCT GCCCTTCGAC AACCTGCACG ATGACCCCTG TCTCCTCACC
AACCGCTCGG CGCGCATCCC CTGCTTCCTG GCAGGTGACA CCCGATCAAC GGAAACCCCC AAAGTGGCAG
60 CCATGCACAC CCTCTTATG CGAGAGCACA ACCGGCTGGC CACCGAGCTG AGACGCTGA ATCCCCGGTG
GAATGGAGAC AAACGTGACA ATGAGGCTCG GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA
GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CCGGCCAGGA GAACCTGGG GCACTACAGG GGGTACTGCT

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- CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCTGGC CTTCGGCTTT GGCCACACAA TGCTCCAGCC
 CTTTCATGTTT CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC ATGTCCCCTACT TAGCTCTGCC
 TTCTTTGCCA GCTGGCGGAT CGTGTATGAA GGGGGCATCG ACCCCATCCT CCGGGGCTC ATGGCCACCC
 CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG
 5 GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGGTACAAT
 GCTTGGAGGC GCTTCTGTGG GCTCTCCAG CCCCAGGAATT TGGCACAGCT TAGCCGGGTG CTGAAAAACC
 AGGACTTGGC AAGGAAGTTC CTGAATTTGT ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT
 CGCTGAGCCT CTTTGTCCGG GGGCTCGAGT GGGGCCTCTT CTGGCTTGTC TGTCGAGAA CCAGTTCAGA
 AGAGCCGAGA CGGAGACAGG TTCTGGTGGC AGAACGAGGT GTTTTACCA AAGACACGCG AAGGCCCTGA
 10 GCAGAAATTC CTTGTCTCGA ATTATATGTG ACAATACCGG TATCACCACG GTTTCAAGGG ACATCTTCAG
 AGCCAACATC TACCCTCGGG GCTTTGTGAA CTGCAGCCGT ATCCCCAGGT TGAACCTATC AGCCTGGCGA
 GGGACATGAG GCTTCTGCAG GAGTCTATCC CAAGTCTCCA ACTTTTGGAG ACAAGGGGAA GGGGAGGACC
 ATGAGGCTGC CTTGTCTCCC TGGAGCAAGT GCAGGCTCGT GACGCTTCTG CTGGCTACAG CTCAGAGCTG
 GGTTCCTCCAG CCAGGAGTGA AGGCTGGGGG CTCCTATCAG CAATGGACCT TCCGCCTTGG GAGCCTCTTA
 15 GGTATTAGGC TATGAATCAG CGCCACGTGC AAAGGCTTGG GAGCCAAGCC ATGTGCTCTT GCACCCAGG
 CAAGAAAAGT CAGCTGGAGG GTTTACAGCA CTTTCTACTG TTCCCAGCC CTCCCTCCCC TCCCTACCA
 TGACTAAGAG ACCACTCGGT CCTAGCCTCC AGACACCCCA CAATACTCCT CTGAGCCTGA GGCCAGGCAG
 CATGCTCTGC TTCTACCAAT AAAGCACTGC CGGAATTC-3' (FRAG. NO:_) (SEQ. ID no:2490)
 5'-TC GGC CTG GTC CCG G-3' (FRAG. NO: 1727) (SEQ. ID NO:1740)
 20 5'-TGG GGG TTT CCG TTG-3' (FRAG. NO: 1728) (SEQ. ID NO: 1741)
 5'-TG GTC CCG GBG BGC -3' (FRAG. NO: 1729) (SEQ. ID NO: 1742)
 5'-GCG CTC GGC CTG GTC CCG G-3' (FRAG. NO:1053) (SEQ. ID NO:1061)
 5'-GGG TCT CCT CTT GTT GTT GC-3' (FRAG. NO:1054) (SEQ. ID NO:1062)
 5'- TTG CGC CTC CTG CTG GGG GT CC-3' (FRAG. NO:1055) (SEQ. ID NO:1063)
 25 5'-CTC TGT TCT TGT TTT GGG GGC-3' (FRAG. NO:1056) (SEQ. ID NO:1064)
 5'-GGG CCC GGC CGT TGT CTT G-3' (FRAG. NO:1057) (SEQ. ID NO:1065)
 5'-GTT TGG GGG TTT CCG TTG-3' (FRAG. NO:1058) (SEQ. ID NO:1066)
 5'-GGG TTC TCC TGG CCC GGG CCT TGC CC-3' (FRAG. NO:1059) (SEQ. ID NO:1067)
 5'-GGC CGT GGT CCC GGC TTC GTT GC-3' (FRAG. NO:1060) (SEQ. ID NO:1068)
 30 5'-CCT GTC TCC GTC TCG GCT CTT CTG-3' (FRAG. NO:1061) (SEQ. ID NO:1069)
 5'-GGG CCT TGC GCT GTC TTT GGT G-3' (FRAG. NO:1062) (SEQ. ID NO:1070)
 5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC -3' (FRAG. NO:1063) (SEQ. ID NO:1071)

Human Intercellular Adhesion Molecule-1 (ICAM-1)

35 Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-GCG CGG GCC GGG GGC TGC TGG G GGT TGG CCC GGG GTG CCC C GCC GCT GGG TGC CCT CGT CCT CTG
 CGG TC GTG TCT CCT GGC TCT GGT TCC CC GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C GCT CCC GGG
 TCT GGT TCT TGT GT TGG GGG TCC CTT TTT GGG CCT GTT GT GGC GTG GCT TGT GTG TTC TTT TGC CCT
 GTC CTC CGG CGT CCC CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT
 40 TGC CBG GTC CTG GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG
 GBG CCB TBG CGB GGC TGB G-3' (FRAG. NO: 1730) (SEQ. ID NO: 1743)
 5'-GGG GGC TGC TGG G-3' (FRAG. NO: 1731) (SEQ. ID NO:1744)
 5'-T GTC CTC CGG CGT CCC-3' (FRAG. NO:1732) (SEQ. ID NO:1745)
 5'-G CCB TBG CGB GGC TGB G-3' (FRAG. NO: 1733) (SEQ. ID NO: 1746)
 45 5'-CTC TGG GGT GGC CTT C-3' (FRAG. NO:1734) (SEQ. ID NO:1747)
 5'-GCG CGG GCC GGG GGC TGC TGG G-3' (FRAG. NO:1064) (SEQ. ID NO:1072)
 5'-GGT TGG CCC GGG GTG CCC C-3' (FRAG. NO:1065) (SEQ. ID NO:1073)
 5'-GCC GCT GGG TGC CCT CGT CCT CTG CGG TC-3' (FRAG. NO:1066) (SEQ. ID NO:1074)
 5'-GTG TCT CCT GGC TCT GGT TCC CC-3' (FRAG. NO:1067) (SEQ. ID NO:1075)
 50 5'-GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C-3' (FRAG. NO:1068) (SEQ. ID NO:1076)
 5'-GCT CCC GGG TCT GGT TCT TGT GT-3' (FRAG. NO:1069) (SEQ. ID NO:1077)
 5'-TGG GGG TCC CTT TTT GGG CCT GTT GT-3' (FRAG. NO:1070) (SEQ. ID NO:1078)
 5'-GGC GTG GCT TGT GTG TTC GGT TTC-3' (FRAG. NO:1071) (SEQ. ID NO:1079)
 5'-TGC CCT GTC CTC CGG CGT CCC-3' (FRAG. NO:1072) (SEQ. ID NO:1080)
 55 5'- CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB BTG TCT GGG CBT TGC CBG GTC CTG
 GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CGG GCC GGG GGC TGC TGG GBG CCB TBG CGB
 GGC TGB G-3' (FRAG. NO:1073) (SEQ. ID NO:1081)

Human Vascular Cell Adhesion Molecule 1 (VCAM-1)

Nucleic Acid and Oligonucleotide Fragments

- 60 5'-CCT CTT TTC TGT TTT TCC C CTC TGC CTT TGT TTG GGT TCG CTT CCT TTC TGC TTC TTC C CTG TGT CTC

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CTG TCT CCG CTT TTT TCT TC GTC TTT GTT GTT TTC TCT TCC TTG CTG BGC BBG BTB TCT BGB TTC TGG GGT
GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG
BCC BTC TTC CCB GGC BTT TTB BGT TGC TGT CGT-3' (FRAG.NO:1735)(SEQ.ID NO:1748)

5'-C TGT CGT-3' (FRAG. NO:1736) (SEQ. ID NO:1749)

5 -5'-TGC TTC TTC C-3' (FRAG. NO:1737) (SEQ. ID NO:1750)

HSVCAM1AS1: 5'-CCT CTT TTC TGT TTT TCC C-3' (FRAG. NO:1074) (SEQ. ID NO:1082)

HSVCAM1AS2: 5'-CTC TGC CTT TGT TTG GGT TCG-3' (FRAG. NO:1075) (SEQ. ID NO:1083)

HSVCAM1AS3: 5'-CTT CCT TTC TGC TTC TTC C-3' (FRAG. NO:1076) (SEQ. ID NO:1084)

HSVCAM1AS4: 5'-CTG TGT CTC CTG TCT CCG CTT TTT TCT TC-3' (FRAG. NO:1077) (SEQ. ID NO:1085)

10 HSVCAM1AS5: 5'-GTC TTT GTT GTT TTC TCT TCC TTG-3' (FRAG. NO:1078) (SEQ. ID NO:1086)

CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB
BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GGC BTT TTB BGT TGC TGT CGT(FRAG.
NO:1079)(SEQ. ID NO:1087)

Human Endothelial Leukocyte Adhesion Molecule(ELAM-1)

15 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-BBG TGB GBG CTG BGB GBB BCT GTG BBG CBB TCB TGB CTT CBB GBG TTC TTT TCB CCC GTT CTT GGC TTC
TTC TGT C CGT TGG CTT CTC GTT GTC CC TGT GGG CTT CTC GTT GTC CC CCC TTC GGG GGC TGG TGG GGC
CGT CCT TGC CTG CTG G GTT CTT GGC TTC TTC TGT CCG T TGG CTT CTC GTT GTC CC TGT GGG CTT CTC
GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G CCTGAGACAG AGGCAGCAGT
20 GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC CAAAACGGA AAGTATTTCA AGCCTAAACC
TTTGGGTGAA AAGAACTCTT GAAGTCATGA TTGCTTCACA GTTCTCTCA GCTCTCACTT TGGTGCTTCT
CATTAAAGAG AGTGGAGCCT GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT
TATTGTCAGC AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAAGAAGA GATTGAGTAC CTAAGTCCA
TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG TCTGGGTAGG
25 AACCAGAAA CCTCTGACAG AAGAAGCCAA GAACTGGGCT CCAGGTGAAC CCAACAATAG GCAAAAAGAT
GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG TGGGCATGTG GAATGATGAG AGGTGCAGCA
AGAAGAAGCT TGCCCTATGC TACACAGCTG CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT
AGAGACCATC AATAATTACA CTTGCAAGTG TGACCCTGGC TTCAGTGGAC TCAAGTGTGA GCAAATTGTG
AACTGTACAG CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCAGTCA CCCACTGGGA AACTTCAGCT
30 ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGGAGACCA TGCAGTGTAT
GTCCTCTGGA GAATGGAGTG CTCCTATTCC AGCCTGCAAT GTGGTTGAGT GTGATGCTGT GACAAATCCA
GCCAATGGGT TCGTGAATG TTTCCAAAAC CCTGGAAGCT TCCCATGGAA CACAACCTGT ACATTTGACT
GTGAAGAAGG ATTTGAACTA ATGGGAGCCC AGAGCCTTCA GTGTACCTCA TCTGGGAATT GGGACAACGA
GAAGCCAACG TGTAAGCTG TGACATGCAG GGCCGTCCGC CAGCCTCAGA ATGGCTCTGT GAGGTGCAGC
35 CATTCCCCTG CTGGAGAGTT CACCTTCAAA TCATCCTGCA ACTTCACCTG TGAGGAAGGC TTCATGTTGC
AGGGACCAGC CCAGGTTGAA TGCACCACTC AAGGGCAGTG GACACAGCAA ATCCCAGTTT GTGAAGCTTT
CCAGTGACA GCCTTGTTCA ACCCGAGCG AGGCTACATG AATTGTCTTC CTAGTGCTTC TGGCAGTTTC
CGTTATGGGT CCAGCTGTGA GTTCTCCTGT GAGCAGGGTT TTGTGTTGAA GGGATCCAAA AGGCTCCAAT
GTGGCCCCAC AGGGGAGTGG GACAACGAGA AGCCACATG TGAAGCTGTG AGATGCGATG CTGTCCACCA
40 GCCCCGAAG GGTTTGGTGA GGTGTGCTCA TTCCCTATT GGAGAATTCA CCTACAAGTC CTCTTGTGCC
TTCAGCTGTG AGGAGGGATT TGAATTATAT GGATCAACTC AACTTGAGTG CACATCTCAG GGACAATGGA
CAGAAGAGGT TCCTTCCTGC CAAGTGATAA AATGTTCAAG CCTGGCAGTT CCGGGAAAGA TCAACATGAG
CTGCAGTGGG GAGCCCGTGT TTGGCACTGT GTGCAAGTTC GCCTGTCTG AAGGATGGAC GCTCAATGGC
TCTGCAGCTC GGACATGTGG AGCCACAGGA CACTGGTCTG GCCTGTCTG TACCTGTGAA GCTCCCACTG
45 AGTCCAACAT TCCCTTGGTA GCTGGACTTT CTGCTGCTGG ACTCTCCCTC CTGACATTAG CACCATTCTT
CCTCTGGCTT CGGAAATGCT TACGCAAACC AAACAAATTT CTCTCTGCGA CCAGCTGCGA AAGCTTGA

GAGGCCAAAC GTTTTGAAC TATAAAAGCA TAAATGCAAA CACACAAAGG TATAATTTTA TGAATGTCTT
 TGTTGGAAAA GAATACAGAA AGATGGATGT GCTTTGCATT CCTACAAAGA TGTTTGTGAG ATGTGATATG
 TAAACATAAT TCTTGTATAT TATGGAAGAT TTTAAATTCA CAATAGAAAC TCACCATGTA AAAGAGTCAT
 CTGGTAGATT TTAAACGAAT GAAGATGTCT AATAGTTATT CCCTATTTGT TTTCTTCTGT ATGTTAGGGT
 5 GCTCTGGAAG AGAGGAATGC CTGTGTGAGC AAGCATTAT GTTTATTTAT AAGCAGATTT AACAATTCCA
 AAGGAATCTC CAGTTTTCAG TTGATCACTG GCAATGAAAA ATTCTCAGTC AGTAATGCC AAAGCTGCTC
 TAGCCTTGAG GAGTGTGAGA ATCAAAACTC TCCTACACTT CCATTAACCTT AGCATGTGTT GAAAAAATAA
 GTTTCAGAGA AGTTCTGGCT GAACACTGGC AACGACAAAG CCAACAGTCA AAACAGAGAT GTGATAAGGA
 TCAGAACAGC AGAGGTTCTT TTAAAGGGGC AGAAAACTC TGGGAAATAA GAGAGAACAA CTACTGTGAT
 10 CAGGCTATGT ATGGAATACA GTGTTATTTT CTTTGAAATT GTTTAAGTGT GTTAAATATT TATGTAAACT
 GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGGTTTGT GTTTGAGTTT TAITGAGAAT TTTAAATTAT
 AACTTAAAT ATTTTATAAT TTTTAAAGTA TATATTTATT TAAGCTTATG TCAGACCTAT TTGACATAAC
 ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT GATCAAAATT TTTACCTATT ATGCATTTGA TATATAAATA
 AGTATATAAA TGCACACACA GACACAGCAA TGATGGTGAA CAGTCTTCAT ACAATTATAT GGATGAATCT
 15 CATAAAATGC TGAGTTAAAG AAATCAGACC AAAGAACATA TACTGAAAGA TTCTCTCTAT ATACAAAGTT
 CAAAAATAGG TGGACCAATT CATGGTGGTG TTAGAAATCA GAAGAGAGGC TACCTTTGTG GGGAGGGGAC
 AGTTTAATGC CCAGAAGCGG TAAATAAGGA ATCCTCTGGG GAGTGGTAAT GATCTGGATG CTGGCTACAG
 GATGTGTTGG TTGTAAAAAT GCATTTTTTT ATATCTAGCT TTTTCCATGT GTATATTATA CTTCAAAGAA
 GTTCAGTTAA TAATTTCTCA TGTCACGTGA GAGTAGCTCA GTTAGCCCTC CCAAGCTCTT GGCTTAATCT
 20 TGTTTTACCT TAAGCCATCA GTCATTTACA AGTAGGAAAA TTCACAGGGA AAGTTAGAGT ATAAAAATCCA
 GAATGAAGGT TTACTGGGTA AGAGTCTCTC CATTTTCCAA AGCCCGTTTA TTTCTTGATT CCAGTCTTA
 AGAAGTCTCA GCATTGTGTC TTTTTCATGT ATCTTACAAG AAGACAGCAT GTGCTTCTAA CACCTGATAC
 ATTGTATCTA CCAGCACTTG GTAAACAGAA AAGAACCACA TTTTCTTGT AGGAGAAATT TGGTGCCTAT
 TTCCTACCAG GCACCAATAA GTGGGACCAA TAGGTGGGAT TAAAGATACA GTAGAAAAGTA TTTAAACTT
 25 GCCAGGGGGC AATAGTCTGA AAATAAGTAA ATTGGTGCTA TAGAATGGAA GTTACAGGCT TCTTTCTTTT
 TTCCACAAG ATCTGCTCCT TGAGCCCCTA GAGACTTTTC TGTCTGTTAC TGTTCCTTCA TTCCTCATCT
 GCAGAGCCAG CCCTGAGAAG TGCAGACCAA AGCCAGGGAA GGCTCTGCAA AGATGTACAA ATGGAAGTCA
 CCTTAATAAC CTCTGACTGC TGCGCATAAT ACATTTCACT CAAAAGAGGG GTTAAACAAT GGAACAGAAT
 ACAGAGGCCA GAAATAATGC TGAACACTGA CAACCATCTG ATCTTTGACA AAATCCACAA AAACAAGCAA
 30 TGGAGAAAAG ACTCCCTATT CCATAATGGT GCTGGGATAA CTGTCTAGCT ATATACAGAA GATTGAACCT
 GGGCCCCTTC CTACATCAT ATACAAAAAA TAACTCAAGA TGGAGTAAAG ACTTAAATCT AAAACCAAAC
 ACTATAAAAA CCCTGGAAGA TAGCCTGGGA AATACCATTG TGGACATAGG ACCTGGCAAA GACTTCATGA
 CAAGACACCA AAAGCAATAG CAACAAAAAC CAAATTGACT AATGAACTA ATGAACTCT TTAGTTGTAC
 AACAGATAGT TTATCTGTAC AACAAAATAA ACTATCAACA GAGTAAACAA CCTACAGAAT GGAAAAATTT
 35 TTTGCAAACT TTGCATCTGA CAAAGGTCTA ATATCCAGAA TCTATAAGGA ATTTAAACAA ATTTACAAGC
 AAAAAAATGA CCTCATTAAG AAGTGGGCAA AGGACATGAA CAGATGCTTT TCAAAATAAG ACATTACAC
 ATCCAACAAC CATATGAAAA GATGTTTAAAC ATCTAATC ATTAGAGGAA TACAAATCAA AAGCATAATA
 AGATACCATC TAATACCAGT AGGAATGACT ACTATTAAAA AGTCAGACAA TAACAGATGC TGGTGAAGGT
 TGTGGAGAAA AGGGAATGTT TATGCACTGC TAGTGGGAAT GTAAACTAGT TCAGCCATTG TGGAAGAGAG
 40 TGTGGTGATT CCTCAAAGAA TGTA AACCG AACTGCCTTT CAATCCAGCA ATCCCATAT TGGATATACA
 CCAAAGGAA TAGAAATTGT TTTACCGTAA AGGCGCATGC ATGCATATGT TCATTACAGC ACTATTTACG
 ATAGCAAAGA CATGGAATCG TCTAAATGCC CATCAGTGGT AGACTAGCTA AAAAAAATAA AATGTGGTAC
 ATATACATCA CAGAATAGTA TGCAGCCATA AAAATGAACA AGATCATCAT GTCTTTTGCA GCAACATGGA
 TGTAAGTTGGA GGCCATTATC CTAAGCAAAAT TAATGCAGGA GAAGGGAACA ATAGACATTG GACCTACTTG
 45 TATAAGTGAC AGCTAAATAT TGAGTACACA TGGACACAAA CATAGGACAC TGTGCTTATT ACCTGGGTGA
 AGAATAGAGG GTGGGAGGAG GGTGAGGATC AAAAAAGTACC CATAGGACAC TGTGCTTATT ACCTGGGTGA
 TGAAATAATT TGCACACCAA ACCCTGTGA CACACAATTT ACCTATATAG AAAACCTGTG CATGTACCCC
 TGAACCTAAA AGTTAATGGT GGGGGGGTGG GGTAAAGCTA CTTTGTGGTA TAAATCTGAG CATTATATT
 AAAATAAAAT ATTTACCTCA TTAGAGTAAT TAACATTAT TAAGCAAAGA GCCAAGTACC TTACACACAT
 50 GATGTTTAAAT CTCACAATGA TCTTTAATCT CATAACAACC GTCCATTGTA TGTACATATG TGGAAATTGA
 GCCTTGGAGA GATTAATGTC ATGGGGCATG CCATTTGACT AGAACTGGA AGCATCAGGA TTTAACTCA
 GTTCTGAAATG GTTTGTAGG CTTTGTGTTT TCCACATTAT AGCATGGCCT GCCATGAAGA ACAGGTCCTT
 TCTGGTGTTT GTCTTGTTTG GTTTAAGTGA AGCAAATATT TATTTAAATA TTCAAGATAT GCTGTAAAT
 55 TTTTACTCAA AAATTTGAGT ACAGTATGGA TCTTCTGAAG CCAAATAACT CTTATTCAAT GCTTAGTTGA
 GAAATTTTAT GGAGTAGTTC TCAATTTTTA TGTAGTTCCA CTGCAAAGGT AAGTCTTATG GAAAGATTCA
 CTGTAATTTT TTTTCTCAT TTGGACATCA GCTTTTTCTT TTCCTCAGAC CCGCTGAAAG ATAATTTTTA
 AAATAAAAAAC CTGTGTTTTA TATCAAGTGG GGACATTTTT TCCAAATGAA AACCGTGTAT TCATTTTATA
 TGATAAAATC AATGTTATTA TTTTAAAAAT TTTGATTTAA AAATCATTA AATAAAATTT TCAGATATTA
 60 CCTGAAATTC TACCATCCAG AGATAATAGT GCTTAAAGAT TTGATATATA GACACACACA CATATATACA
 TATATATCAT CCTAAACTTC TTTGTATAAA TGTATATAAA GTTTTAAATA AAAACTAGGA GATTAATGCC
 CTTTGAATGA AAATAAAATC AATGTGTATG CTTTAAACATC TTGCCTTTAC TTTATAACAT TTATCACAGC
 AGTCATGAGA TAATGATTTA CATGGTCATT GTTAGTAAGC TAATAGCTAA GTGCATGAAC TCTGGAGCTA

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GCCTCCCTGG ATTTTAATCC CAGATCTGTC ACTGACCAGC TGAGCAATAC TAGGTAAAT GCTCTTGTTCT
 CTTAGTTTCT TCATCTGTAA AATAGAGATA AAAATAATAT CCACCTCATA GGATTGGTGT GAGCATTAAA
 TGAGCATACG TATGTAGGCC ACTTAACAAC AATGCCTTCA CATACTGAAC ACAAATATAC GAGCTGTTGT
 CTTATTGGGC TCATGTTTTT CCTACCACTA AGCCGCATGC ATGCAAGGAC CATGTTGGTT TTGTTCCACA
 5 TTGCATCCCC AACCTGGTAT ACAGTGTGCA TTCAATAGTT GTTGACTATT ATTACTAGTG GCATTTAACA
 AATACTCTGTT AAATGAGTGA AGAAATACCC ATTTACTGCA AGTGTGTCTA ATATTGATGG CATAATGGGG
 GAAACTCAAA CTCTGGAGTC AAACAGGTTT TAAAACCTTA TTCCTCATC CTCAGTTATT GACGTTTTTT
 TTTTGGCAGG TGTGTGTGTG GGACAACCTTA TTGAACCTTT CTGAATTTCC AGCTTCGCAT ATATAAAATA
 GAGATAGTGA TTCAATCTTG CAATGTATGG ATTTGAGACA ATTGTGTAAG TTTATCAATA AATAGTAGCT
 10 ATTTTTGTAT AAGTATTACA TATAATATCC AGGCCACTGC TTTGCATAAC CCAAAAAGGGG CACCATTATC
 GCAGAAATACA ACATAAATGG TGTCCCTGGA GCAGTGCAGT ATAGGAACCC TGAGGGGACC TACAGTATAC
 TTTATAGTTC ATAGATTACA AATTATCCCT TTATCAGAGT CTCTCAAGGT TGGATGTATT TGAGGTCCAT
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 15 CACAACAAAT ACCCAGTGAG AGAGGGAGAA GGGAAAGTAAA TGCCTCTGAA TAAGCAAGTT AATGTCAGTA
 GTTGTACTGT ATGCATATTG ATGAACAATA GAGGAACCAA TGTCCAATCA GATGAGCAGG ATATTTGGCA
 ATAACAAGTT GCCTTTGAGG AAAAATGATT TTCTTGGCAA GTTCTTTATC AGCATTACAA AGCTAAAAAGC
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 35 CTAGTGCTTC TGGCAGTTTC CGTTATGGGT CCAGTGTGTA GCTCTCTGT GAGCAGGGTT TTGTGTGAA
 GGGATCCAAA AGGCTCCAAT GTGGCCCCAC AGGGGAGTGG GACAACGAGA AGCCACATG TGAAGCTGTG
 AGATGCGATG CTGTCCACCA GCCCCGAAG GGTTTGGTGA GGTGTGCTCA TTCCCTATT GGAGAATTCA
 CCTACAAGTC CTCTTGTCCT TTCAGCTGTG AGGAGGGATT TGAATTATAT GGATCAACTC AACTTGAGTG
 CACATCTCAG GGACAATGGA CAGAAGAGGT TCCTTCTGCT CAAGTGGTAA AATGTTCAAG CCTGGCAGTT
 40 CCGGGAAAGA TCAACATGAG CTGCAAGTGG GAGCCCGTGT TTGGCACTGT GTGCAAGTTC GCCTGTCTG
 AAGGATGGAC GCTCAATGGC TCTGCAGCTC GGACATGTGG AGCCACAGGA CACTGGTCTG GCCTGTCTACC
 TACCTGTGAA GCTCCCAGT AGTCCAACAT TCCCTTGCTA GCTGGACTTT CTGCTGCTG ACTCTCCCTC
 CTGACATTAG CACCATTCTT CCTCTGGCTT CGGAAATGTA TACGGAAAGC AAAGAAATTT GTTCTTGCCA
 45 GCAGCTGCCA AAGCCTTGAA TCAGACGGAA GCTACCAAAA GCCTTCTTAC ATCCTTTAAG TTCAAAAGAA
 TCAGAAACAG GTGCATCTGG GGAAGTAGAG GGATACACTG AAGTTAACAG AGACAGATAA CTCTCCTCGG
 GTCTCTGGCC CTCTTGCTCT ACTATGCCAG ATGCCTTTAT GGCTGAAACC GCAACACCCA TCACCACTTC
 AATAGATCAA AGTCCAGCAG GCAAGGACGG CCTTCAACTG AAAAGACTCA GTGTTCCCTT TCCTACTCTC
 50 AGGATCAAGA AAGTGTGGC TAATGAAGGG AAAGGATATT TTCTTCCAAG CAAAGGTGAA GAGACCAAGA
 CTCTGAAATC TCAGAATTCC TTTTCTAACT CTCCCTTGCT CGCTGTAAAA TCTTGGCACA GAAACACAAT
 ATTTGTGGC TTTCTTTCTT TTGCCCTTCA CAGTGTTTCG ACAGCTGATT ACACAGTTGC TGTCTAAGA
 ATGAATAATA ATTATCCAGA GTTTAGAGGA GGGTTGTTAA TGGTGCAAAT CCTACTGAAT GCTCTGTGCG
 55 ATGTTGAATG CCCACAGGCA AATGCATGGA ATCCCTATGG GATTCAAGTG TTCTTAAAGA GTTCTTAAAG
 AGGGTTACTA TGCACAATTT AATCACTTTC ATCCCTATGG GATTCAAGTG TTCTTAAAGA GTTCTTAAAG
 ATTGTGATAT TTTTACTTGC ATTGAATATA TTATAATCTT CCATACTTCT TCATTCAATA CAAGTGTGGT
 AGGGACTTAA AAAACTTGTA AATGCTGTCA ACTATGATAT GGTAAAAGTT ACTTATTCTA GATTACCCCC
 60 TCATTGTTTA TTAACAAATT ATGTTACATC TGTTTTAAAT TTATTTCAAA AAGGGAAACT ATTGTCCCTT
 AGCAAGGCAT GATGTTAACC AGAATAAAGT TCTGAGTGT TTTACTACAG TTGTTTTTTG AAAACATGGT
 AGAATTGGAG AGTAAAAACT GAATGGAAGG TTTGTATATT GTCAGATATT TTTTCAGAAA TATGTGGTTT
 CCACGATGAA AAACCTCCAT GAGGCCAAAC GTTTTGAAC AATAAAAGCA TAAATGCAAA CACACAAAGG
 TATAATTTTA TGAATGCTCT TGTTGGAAAA GAATACAGAA AGATGGATGT GCTTTGCATT CTACAAAGG
 TGTGTGTCAG ATGTGATATG TAAACATAAT TCTTGATAT TATGGAAGAT TTAAATTCA CAATAGAAAC
 TCACCATGTA AAAGAGTCAT CTGGTAGATT TTAAACGAAT GAAGATGTCT AATAGTTATT CCCTATTTGT
 TTTCTTCTGT ATGTTAGGGT GCTCTGGAAG AGAGGAATGC CTGTGTGAGC AAGCATTTAT GTTTATTTAT
 AAGCAGATTT AACAATTCCA AAGGAATCTC CAGTTTTTCAG TTGATCACTG GCAATGAAAA ATTCTCAGTC
 AGTAATTGCC AAAGCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAAACTC TCCTACACTT CCATTAACCT

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 004040" 6294560

- AGCATGTGTT GAAAAAAAAA GTTTCAGAGA AGTTCTGGCT GAACACTGGC AACGACAAAG CCAACAGTCA
 AAACAGAGAT GTGATAAGGA TCAGAACAGC AGAGGTCTT TTAAAGGGGC AGAAAACTC TGGGAAATAA
 GAGAGAACAA CTACTGTGAT CAGGCTATGT ATGGAATACA GTGTTATTTT CTTTGAAATT GTTTAAGTGT
 TGTAATATT TATGTAAACT GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGGTTTGT GTTTGAGTTT
 5 TATTGAGAAT TTAAATTAT AACTTAAAT ATTTATAAT TTTTAAAGTA TATATTATT TAAGCTTATG
 TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT-3' (FRAG.NO:)(SEQ.ID NO:2479)
 5'-CCT TGC CTG CTG G-3' (FRAG. NO: 1739) (SEQ. ID NO: 1752)
 5'-GTT GTC CC-3' (FRAG. NO: 1740) (SEQ. ID NO:1753)
 5'-GTT CTT GGC TTC TTC TGT C-3' (FRAG. NO:1080) (SEQ. ID NO:1088)
 10 5'-GGC TGG TGG-3' (FRAG. NO:1083) (SEQ. ID NO:1092)
 5'-CGT TGG CTT CTC GTT GTC CC-3' (FRAG. NO:1081) (SEQ. ID NO:1089)
 5'-TGT GGG CTT CTC GTT GTC CC-3' (FRAG. NO:1082) (SEQ. ID NO:1090)
 5'-CCC TTC GGG GGC TGG TGG-3' (FRAG. NO:1083) (SEQ. ID NO:1091)
 5'-GGC CGT CCT TGC CTG CTG G-3' (FRAG. NO:1084) (SEQ. ID NO:1093)

15 Human P Selectin Fragments

- 5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC
 TTT CTT TTC-3' (FRAG. NO: 1741) (SEQ. ID NO: 1754)
 5'-TCC TTT CTT TTC-3' (FRAG. NO: 1742) (SEQ. ID NO: 1755)]
 5'-CTC CTT TT-3' (FRAG. NO:1743) (SEQ. ID NO:1756)
 20 5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3'(FRAG.NO:1085)(SEQ. ID NO:1094)
 5'-TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' (FRAG. NO:1086) (SEQ. ID NO:1095)

Human Endothelial Monocyte Activating Factor

Nucleic Acid & Antisense Oligonucleotide Fragments

- 5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC
 25 TTT CTT TTC-3' (FRAG. NO: 1744) (SEQ. ID NO: 1757)
 5'-CC TTT CTT TTC (FRAG. NO: 1745) (SEQ. ID NO: 1758)
 5'-CTG TTC CTC CTT TT-3' (FRAG. NO:1746) (SEQ. ID NO:1759)
 5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3'(FRAG.NO:1087)(SEQ. ID NO:1096)
 5'-TTG CTG TTT TTT CTC CTT CTT CTC TCC TTT CTT TTC-3' (FRAG. NO:1088) (SEQ. ID NO:1097)

30 Human IL3* Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG TGT CGC GTG G GTG CGG CCG TGG CC GGC GGB CCB
 GGB GTT GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC (FRAG. NO:
 1747) (SEQ. ID NO: 1760)]
 5'-G GBG GCB CTC-3' (FRAG. NO: 1748) (SEQ. ID NO: 1761)
 35 5'-GT GGG GCT CTG-3' (FRAG. NO:1749) (SEQ. ID NO:1762)
 HUMIL3AAS1: 5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG-3' (FRAG.NO:1089)(SEQ.ID NO:1098)
 HUMIL3AAS2: 5'-TGT CGC GTG G GTG CGG CCG TGG CC-3' (FRAG. NO:1090) (SEQ. ID NO:1099)
 GGC GGB CCB GGB GTT GGB GCB GGB GCB GGB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC
 (FRAG. NO:1091) (SEQ. ID NO:1100)

40 Human IL3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-CTCTTCCCCGGGCTCTT (FRAG. NO:1097) (SEQ. ID NO:1106)
5'-GCGCTGGGGGTGCTCC (FRAG. NO:1098) (SEQ. ID NO:1107)
5'-CGTGTGTTTGCGCCCTCCTGGTCGC (FRAG. NO:1099) (SEQ. ID NO:1108)
5'-GCTGTGCTTTTGG (FRAG. NO:1100) (SEQ. ID NO:1109)
5'-GGCCGGCTTTGCCCCCTCCC (FRAG. NO:1101) (SEQ. ID NO:1110)
5'-GGCGCTGGCCCGGCC (FRAG. NO:1102) (SEQ. ID NO:1111)
5'-TTCCTGGGCTGCGTGCGC (FRAG. NO:1103) (SEQ. ID NO:1112)
5'-GTTCTGTTCTTCTCCTGGC (FRAG. NO:1104) (SEQ. ID NO:1113)
5'-GCB GGB GBC BGG GCB GGG CGB TCB GGB GCB GCG TGB GCC BBB GGB GGB CCB TCG GGB BCG CBG CTC
10 CGG BBC GCB GGB 5'-CBG BGG TGC C (FRAG. NO:1105) (SEQ. ID NO:1114)

Human IL-4 Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-CTC TGG TTG GCT TCC TTC GCC GGC BCB TGC TBG CBG GBB GBB BGG GGG BBG CBG TTG GGB GGT
GBG BCC CBT TBB TBG GTG TCG B-3' (FRAG. NO: 1753) (SEQ. ID NO: 1766)
5'-GCC GGC BCB-3' (FRAG. NO: 1754) (SEQ. ID NO: 1767)
15 5'-T TCC TTC-3' (FRAG. NO:1755) (SEQ. ID NO:1768)
5'-CTC TGG TTG GCT TCC TTC-3' (FRAG. NO:1106) (SEQ. ID NO:1115)
5'-GCCGCBCTGTGCTBGBGBBBBGBBGBGGGGBBGBGCBGTTGGGBGGTGBGBCCCBTTBBTBGGTGTGCB-3' (FRAG.
NO:1107) (SEQ. ID NO:1116)

Human IL4 Receptor Nucleic Acid and Antisense Oligonucleotide Fragment

- 20 5'-TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT
GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT
GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC TCC CTT CCT CTG TCT TGC CTC CTT CCT CTG GGT CCT
CTT GGC CTG GGC GCT CTT CCC CTC GGG CGG CTG CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT
GCT CCT TCC CTT TCC CCG CTC GTG GGG TTT GCG GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG
25 GTC GGC TGG CTG CTG CTT CGG GCC GCC TGG GCT TCC CTG TGC CCC TTT CCT CTG CTG GGT CCC CCT CCC
GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA GGA CAG AGC CAG GCA AGC ACC CAT GGG GAT CCA
GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC GGC GCT BCB GGB CBG BGC CBG GCB BGC BCC CBT GGG
GBT CCB GGC CCB GCT G -3' (FRAG. NO: 1756) (SEQ ID NO:1769)
5'-TCTGCGC-3' (FRAG. NO: 1757) (SEQ ID NO: 1770)
30 5'-CCT GCT CCT GGG G (FRAG. NO:1758) (SEQ. ID NO:1771)
5'-TCTGCGCGCCCTGCTCC (FRAG. NO:1108) (SEQ. ID NO:1117)
5'-CGCCCGGCTTCTCT (FRAG. NO:1109) (SEQ. ID NO:1118)
5'-CGTGTGGGCTTCGG (FRAG. NO:1110) (SEQ. ID NO:1119)
5'-CCCCGCGCCTCCGTTGTTCTC (FRAG. NO:1111) (SEQ. ID NO:1120)
35 5'-TGCTCGCTGGGCTTG (FRAG. NO:1112) (SEQ. ID NO:1121)
5'-GGTTTCCTGGGGCCCTGGGTTTC (FRAG. NO:1113) (SEQ. ID NO:1122)
5'-TCTGCCGGGTCGTTTTC (FRAG. NO:1114) (SEQ. ID NO:1123)
5'-GGGTGCTGGCTGCG (FRAG. NO:1115) (SEQ. ID NO:1124)
5'-CTTGGTGCTGGGGCTCC (FRAG. NO:1116) (SEQ. ID NO:1125)
40 5'-GGCGGCTGCGGGCTGGGTGGG (FRAG. NO:1117) (SEQ. ID NO:1126)
5'-CTTGGCTGGTTCCTGGCCTCGGG (FRAG. NO:1118) (SEQ. ID NO:1127)
5'-CCTCCTCCTCCTCCTCGCTCCCTTTTCTTCTCT (FRAG. NO:1119) (SEQ. ID NO:1128)
5'-TCCCTGCTGCTCTC (FRAG. NO:1120) (SEQ. ID NO:1129)
5'-TGCCCTCCCTTCCCTCCTGG (FRAG. NO:1121) (SEQ. ID NO:1130)
45 5'-GGTGCTCCTTGGGCCCTGC (FRAG. NO:1122) (SEQ. ID NO:1131)
5'-GGCTGCTCCTTGCCCC (FRAG. NO:1123) (SEQ. ID NO:1132)
5'-CTCTGGGTGCGGCTGGC (FRAG. NO:1124) (SEQ. ID NO:1133)
5'-GGGGCGTCTCTGTGC (FRAG. NO:1125) (SEQ. ID NO:1134)
5'-CTGGCCTGGGTGCC (FRAG. NO:1126) (SEQ. ID NO:1135)
50 5'-GCCTCTCTGGGGGGGTGGCTCCTGTCC (FRAG. NO:1127) (SEQ. ID NO:1136)

5'-GTT CCC AGA GCT TGC CAC CTG CAG CAG GAC CAG GCA GCT CAC AGG GAA CAG GAG CCC AGA GCA AAG
CCA CCC CAT TGG GAG ATG CCA AGG CAC CAG GCT G (FRAG. NO:1138) (SEQ. ID NO:1147)

5'-GTT CCC BGB GCT TGC CBC CTG CBG CBG GBC CBG GCB GCT CBC BGG GBB CBG GBG CCC BGB GCB BBG
CCB CCC CBT TGG GBG BTG CCB BGG CBC CBG GCT G-3' (FRAG. NO:1139) (SEQ. ID NO:1148)

5 Human IL5* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCCCTGTTTC CCCCTTTTCG TTCTGCGTTT GCCTTTGGCG TTTTGTGTTT GTTTTCTCTC TCCGTCTTTC
TTCTCCCCT GTGGGBBTTT CTGTGGGGBT GGCBTBCBCG TBGGCBGCTC CBBGBGCTBG CBBBCTCBBB
TGCBGBBGB TCCTCBTGGC TCTGBBBCCG TGGGAATTTC TGTGGGGBTG GCATACACGT AGGCAGCTCC
AAGAGCTAGC AAACCTCAAAT GCAGAAGCATC CTCATGGCTC TGAAACG-3' (FRAG. NO: 1759) (SEQ. ID NO:

10 1772)

5'-GCC CCG GG-3' (FRAG. NO: 1760) (SEQ. ID NO: 1773)

5'-G GGT TTC T-3' (FRAG. NO: 1761) (SEQ. ID NO: 1774)

5'-GTG GGG BTG GC-3' (FRAG. NO: 1762) (SEQ. ID NO:1775)

5'-CCB BGB GCT BGC-3' (FRAG. NO: 1763) (SEQ. ID NO: 1776)

15 5'-TCC CTG TTT CCC CCC TTT-3' (FRAG. NO:1140) (SEQ. ID NO:1149)

5'-CGT TCT GCG TTT GCC TTT GGC-3' (FRAG. NO:1141)(SEQ. ID NO:1150)

5'-GTT TTT TGT TTG TTT TCT-3' (FRAG. NO:1142)(SEQ. ID NO:1151)

5'-CTC TCC GTC TTT CTT CTC C-3' (FRAG. NO:1143) (SEQ. ID NO:1152)

5'-CCT CCT GCC TGT GTC CCT GCT CCC C-3' (FRAG. NO:1144) (SEQ. ID NO:1153)

20 5'-GAG GGT TTC TGG CTT CCT CTC T-3' (FRAG. NO:1145) (SEQ. ID NO:1154)

5'-TGT CTC TCT GTC CTT TTG TT-3' (FRAG. NO:1146) (SEQ. ID NO:1155)

5'-TGT TGT GCG GCC TGG TGC TGC CCT GCC CCG GG-3' (FRAG. NO:1147) (SEQ. ID NO:1156)

5'-GTG GGA ATT TCT GTG GGG BTG GCA TAC ACG TAG GCA GCT CCA AGA GCT AGC AAA CTC AAA TGC AGA
AGC ATC CTC ATG GCT CTG AAA CG-3' (FRAG. NO: 1764) (SEQ. ID NO: 1777)

25 5'-GTG GGB BTT TCT GTG GGG BTG GCB TBC BCG TBG GCB GCT CCB BGB GCT BGC BBB CTC BBB TGC BGB BGC
BTC CTC BTG GCT CTG BBB CG-3' (FRAG. NO:1148) (SEQ. ID NO:1157)

Human IL-5 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTCAGTGGCC CCCAAAAGGA TGAGTAATAC ATGCGCCACG ATGATCATAT CCTTTTACT ATGAGGCCGT
GTCTGTCTGTG TCTTTCCTTT GCTCTTGTTG TGTCTTTGCT GTGCCCTGCC TCTCTGCCCG TGTCTGTCTG
30 GTCTTTCCTT TGCTCTTGGT GTGTCTTTGC TGTGCCCTGC CTCTCTGCC CGTGTCTGTC GTGTCTTTCC
TTTGCTCTTG GTGTGTCTTT GCTGTGCCCT GCCTCTCTGC-3' (FRAG. NO: 1765) (SEQ. ID NO: 1778)

5'-CCG TGT C-3' (FRAG. NO: 1766) (SEQ. ID NO: 1779)

5'-GCCCTGCC-3' (FRAG. NO: 1767) (SEQ. ID NO: 1780)

5'-CCG TGT CTG TCG TGT CT-3' (FRAG. NO:1149) (SEQ. ID NO:1158)

35 5'-TTCCTTTGCTCTTG-3' (FRAG. NO:1150) (SEQ. ID NO:1159)

5'-CTCTCTCTTCTCT-3' (FRAG. NO:1151) (SEQ. ID NO:1160)

- 5'-GTCCCTCGGCCCCGCGCCGCTCGGCTCCTCTCCC-3' (FRAG. NO:1155) (SEQ. ID NO:1164)
 5'-TCTGGCCCCGGCTC-3' (FRAG. NO:1156) (SEQ. ID NO:1165)
 5'-GGGGCGGGGCGGGGCGGTGGGCGGGC-3' (FRAG. NO:1157) (SEQ. ID NO:1166)
 5'-GGCGCTGCCCTGCGC-3' (FRAG. NO:1158) (SEQ. ID NO:1167)
 5'-GCGGCGCTGGCCCC-3' (FRAG. NO:1159) (SEQ. ID NO:1168)
 5'-TGCTGGCCGTCGGCTGCGCGTCTGGCTGCCCT-3' (FRAG. NO:1160) (SEQ. ID NO:1169)
 5'-GCTGGCCGCGCCGGG-3' (FRAG. NO:1161) (SEQ. ID NO:1170)
 5'-GCCTGTCCGCTCTGCGGG-3' (FRAG. NO:1162) (SEQ. ID NO:1171)
 5'-CGCTGTCTCCTGGC-3' (FRAG. NO:1163) (SEQ. ID NO:1172)
 5'-TTGTCTTCCGGCTCT-3' (FRAG. NO:1164) (SEQ. ID NO:1173)
 5'-TCTGCTGGGGTGGG-3' (FRAG. NO:1165) (SEQ. ID NO:1174)
 5'-GCTGGGCGGCCGGCCGGT-3' (FRAG. NO:1166) (SEQ. ID NO:1175)
 5'-GCTGGGGCTCCTCGGGGGG-3' (FRAG. NO:1167) (SEQ. ID NO:1176)
 5'-GGGGGCTCTTCCGG-3' (FRAG. NO:1168) (SEQ. ID NO:1177)
 5'-GCTGTCTCCCTCCGGG-3' (FRAG. NO:1169) (SEQ. ID NO:1178)
 5'-GCGGGGGTTTCTGGCC-3' (FRAG. NO:1170) (SEQ. ID NO:1179)
 5'-GTGGGGGTCTTGCC-3' (FRAG. NO:1171) (SEQ. ID NO:1180)
 5'-TGGCCTCCGGGCTCC-3' (FRAG. NO:1172) (SEQ. ID NO:1181)
 5'-TGCTGTCTTGCCCTCCTTC-3' (FRAG. NO:1173) (SEQ. ID NO:1182)
 5'-TCTGGTCGGTTGTGGCTCG-3' (FRAG. NO:1174) (SEQ. ID NO:1183)
 5'-GGGCTCCGTGGGTCCCTGGC-3' (FRAG. NO:1175) (SEQ. ID NO:1184)
 5'-GCCCGTTTGTGTTTGTGTC-3' (FRAG. NO:1176) (SEQ. ID NO:1185)
 5'-TTTTCCCCTGGCGT-3' (FRAG. NO:1177) (SEQ. ID NO:1186)
 5'-CCCTGTGCCCCCTCCTCTCCTTCTCTGCTTCTC-3' (FRAG. NO:1178) (SEQ. ID NO:1187)
 5'-GCTCTCCTTTGTGGG-3' (FRAG. NO:1179) (SEQ. ID NO:1188)
 5'-GCCCTCCCTGCTGCT-3' (FRAG. NO:1180) (SEQ. ID NO:1189)
 5'-CTTGGTTTGGGCT-3' (FRAG. NO:1181) (SEQ. ID NO:1190)
 5'-TTTTTCTCTCCTCCTTTTC-3' (FRAG. NO:1182) (SEQ. ID NO:1191)
 5'-GTGCGTGGGCTCC-3' (FRAG. NO:1183) (SEQ. ID NO:1192)
 5'-GCACGCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG
 GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCTT CCTCGGCTAC CACTCCATGG TCCCGCAGAG
 GCGGACAGGC-3' (FRAG. NO:1185) (SEQ. ID NO:1194)
 5'-GCBGCGCTCT TGCCBCCTCC TGCGCBGGGC BGCCTTGG GGCCBGCGCC GCTCCCGGCG CGGCCBGCGB
 GGCBCGCBG CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCBGB
 GGCGBCBGG C-3' (FRAG. NO:1187) (SEQ. ID NO:1196)

Human IL-6 Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-GGGGGTGGCT TCTGCCGCG TCTTGGGCC GTCCCGTCCC TCGGCCCGCG GCCGCGCTCG GCTCCTCTCC
 CTCTGGCCCG GCTCGGGGCG GGGCGGGGCG GTGGGCGGGC GGCGCTGCC TGCGCGCGGC GTGGCCCCCT
 GCTGGCCGCT GGCTGCGCG TGCTGGCTGC CTTGCTGGCC GCGCCGGGGC CTGTCCGCT CTGCGGGGCG
 40 TGTCTCCTGG CTGTCTTCC GGCTCTTCT GTGGGTGGG GCTGGGCGGC CGGCCGGGTG CTGGGGCTCC
 TCGGGGGGGG GGGCTCTTCC GGGCTGTCT CCTCCGGGGC GGGGGTTTCT GGCCGTGGGG GTCTTGCTG
 GCCTCCGGGC TCCTGCTTGT CTTGCCTTCC TTCTGTGGT GGTGTGGCT CGGGGTCCG TGGGTCCCTG
 GCGCCCGTTT GTGTTTGTG TTTTCCCTG GCGTCCCTGT GCCCTCTCC TCTCTTCTCT CTGCTTCTCG
 CTCTCCTTTG TGGGGCCCTC CTGCTGCTC TTGGTTTTGG GCTTTTTTTC TCTTCTCTCT TTTTCGTGCG
 45 TGGGCTCC GCACGCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG
 CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCTT CCTCGGCTAC CACTCCATGG
 TCCCGCAGAG GCGGACAGGC GCBGCGCTC TTGCCBCTC CTGCGCBGG CBGCGCCTTG GGGCCBGCGB
 CGTCCCGGC GCGGCCBGB GGGCBGCCB CBGCGCGCB CCGBCGCCB GCBTGCTTCC TCCTCGGCTB
 CCBCTCCBTG GTCCCGCBGB GGCGBCBGG C-3' (FRAG. NO:1772) (SEQ. ID NO:1785)
 50 5'-GGGGBGG-3' (FRAG. NO:1773) (SEQ. ID NO:1786)
 5'-GBBGGCBG CBGGC-3' (FRAG. NO:1774) (SEQ. ID NO:1787)
 5'-CCBGBGCBG CCCC-3' (FRAG. NO:1775) (SEQ. ID NO:1788)
 5'-BGGG BGBBGGCBBC-3' (FRAG. NO:1776) (SEQ. ID NO:1789)
 5'-GCT TCT CTT TCG TTC CCG GTG GGC TCG-3' (FRAG. NO:1188) (SEQ. ID NO:1197)
 55 5'-GTG CCT GTC TGT GTG GGG CGG CT-3' (FRAG. NO:1189) (SEQ. ID NO:1198)
 5'-GTG CCT CTT TGC TGC TTT C-3' (FRAG. NO:1190) (SEQ. ID NO:1199)
 5'-GAT TCT TTG CCT TTT TCT GC-3' (FRAG. NO:1191) (SEQ. ID NO:1200)
 5'-CTCTGGGGG TBCTGGGCB GGBBGGCBG CBGGCBBCB CBGGBGCBC CCBGGGBGB BGGCBCTGG BCCBBGGCG
 CTTGTGBGB BGGBTTCBT BGCTGGGCTC CTGGBGGGB GBTBGBGC-3' (FRAG. NO:1777) (SEQ. ID NO:1790)

60 Human Monocyte-derived Neutrophil Chemotactic Factor

Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-GGGGTGGBBB GGT TTGGBGT BTGTCTTTBT GCBCTGBCBT CTBBGTTCCT TBGCBCTCCT TGGCBBBCT
GCBCTTCBC BCBGBGCTGC BGBBCTCBGG BBGGTGCCB BGBBGCCBC GGCCBGCTTG GBBGTCBTGT
5 5'-GGGGTGGBBB GGT TTGGBGT BTGTCTTTBT GCBCTGBCBT CTBBGTTCCT TBGCBCTCCT TGGCBBBCT
TTCCTGGCTC TTGTCCTTC TCTTGG CCCT TGGC-3' (FRAG. NO:1778) (SEQ. ID NO: 1791)
5'-GGBGT BTG-3' (FRAG. NO:1779) (SEQ. ID NO: 1792)
5'-GCBCTGBCBT CT-3' (FRAG. NO:1780) (SEQ. ID NO:1793)
5'-CCG GTG G-3' (FRAG. NO:1781) (SEQ. ID NO: 1794)
5'-GG CCC TTG GC-3' (FRAG. NO:1782) (SEQ. ID NO: 1795)
10 5'-GCT TGT GTG CTC TGC TGT CTC T-3' (FRAG. NO:1192) (SEQ. ID NO:1201)
5'-TGG TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' (FRAG. NO:1193) (SEQ. ID NO:1202)
5'-TTC TCT TGG CCC TTG GC-3' (FRAG. NO:1194) (SEQ. ID NO:1203)
5'-GGGGTGGBBB GGT TTGGBGT BTGTCTTTBT GCBCTGBCBT CTBBGTTCCT TBGCBCTCCT TGGCBBBCT
GCBCTTCBC BCBGBGC-3' (FRAG. NO:1783) (SEQ. ID NO: 1796)

Human Neutrophil Elastase (Medullasin) Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG
CBGTGCGCGG CCGBCBTGBC GBBGTTGGGC GCBTTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT
GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG CCGGCCCCC BCBTCTCCG BGGCCBGC
5 5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG
GTGCCCCC BGCBCBBGG CCGGCBGGC BCBGGCBBG BGBCBGCGB GTCGGCGGCC GBGGTCTBTG
20 5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG
GTGGGCTGG GGCTCCGGG TCTCTGCCCC TCCGTGCTGG TGGGGCTGGG GTCGGGGG TCTCTGCCCC
TCCGTGCTGG GTGGGCGGC GTCGCGCGC CCCCCCTGC CGGTGGGCT CCGCGCGC GCGGCTGC
CGGCCCCG TGGGTCTGC TGGCGGGTC CGGTCCCG GGTGGGGCG CGBGTGGCG GCCBGGGTC-3'
(FRAG. NO:1784) (SEQ. ID NO: 1797)
5'-GG TGG GGC-3' (FRAG. NO:1785) (SEQ. ID NO: 1798)
25 5'-G GGG CCG -3' (FRAG. NO:1786) (SEQ. ID NO:1799)
5'-GGC CGG GTC CGG G-3' (FRAG. NO:1787) (SEQ. ID NO: 1800)
5'-TGG TGG GGC TGG GGC TCC GGG GTC TCT GCC CCT CCG TGC-3' (FRAG. NO:1195) (SEQ. ID NO:1204)
5'-CGC GTG GGG CCG CGC TCG CCG GCC CCC C-3' (FRAG. NO:1196) (SEQ. ID NO:1205)
5'-CCT GCC GGG TGG GCT CCC GCC GCG-3' (FRAG. NO:1197) (SEQ. ID NO:1206)
30 5'-CGC CGG CCT GCC GGC CCC TC-3' (FRAG. NO:1198) (SEQ. ID NO:1207)
5'-GTG GGT CCT GCT GGC CGG GTC CGG GTC CCG GGG GTG GGG-3' (FRAG. NO:1199) (SEQ. ID NO:1208)
5'-CGC GBG TCG GCG GCC GBG GGT C-3' (FRAG. NO:1200) (SEQ. ID NO:1209)
5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG
CBGTGCGCGG CCGBCBTGBC GBBGTTGGGC GCBTTCBGGG TGGCGCCGCB GBBGTGGCCT CCGCGCBGCT
35 5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBCCGCGC GGBCGTTTBC BTTCGCCBCG
GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG CCGGCCCCC BCBTCTCCG BGGCCBGC
GGTCCCCC BGCBCBBGG CCGGCBGGC BCBGGCBBG BGBCBGCGB GTCGGCGGCC GBGGTCTBTG
GTGGGCTGG GGCTCCGGG TCTCTGCCCC TCCGTGC-3' (FRAG. NO:1788) (SEQ. ID NO: 1801)

Human Neutrophil Oxidase Factor Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-CGGBGTGGG GGTCTGGBC GGCCTGGBG GCBTCCBGGG CTCCCTCCB GTCCTTCTTG TCCGCTGCCB
40 5'-CGGBGTGGG GGTCTGGBC GGCCTGGBG GCBTCCBGGG CTCCCTCCB GTCCTTCTTG TCCGCTGCCB
GCBCCCTTC BTTCBGBGG CTBTGGCCT CCBCCBGGG CBTGTTBGG TBGBBCTBG GBGGCCGCC
TCCBCCBGGG BCBTGGTCT TCTGTCCG TGCTCTCTG GGGTTTCGG TCTGGGTGGG CTTCTCTCT
GGGGCTGTG CTGGGCTCT CTTTTGTT CTGGCCTGGT GCTCTCTGT GCCCTTCCC TTGGGTGTCT
TGTTTTGTG GCCTCCBCCB GGGBCTG-3' (FRAG. NO:1789) (SEQ. ID NO: 1802)
5'-CGGBGTGGG GG-3' (FRAG. NO:1790) (SEQ. ID NO: 1803)
45 5'-GCCBGCBCCC-3' (FRAG. NO:1791) (SEQ. ID NO: 1804)
5'-C CBC CBG-3' (FRAG. NO:1792) (SEQ. ID NO: 1805)
5'-GGC CTC CBC CBG GGB CBT G-3' (FRAG. NO:1201) (SEQ. ID NO:1210)
5'-GTC CTT CTT GTC CGC TGC C-3' (FRAG. NO:1202) (SEQ. ID NO:1211)
5'-TCT CTG GGG TTT TCG GTC TGG GTG G-3' (FRAG. NO:1203) (SEQ. ID NO:1212)
50 5'-GCT TTC CTC CTG GGG CTG CTG CTG-3' (FRAG. NO:1204) (SEQ. ID NO:1213)
5'-GGC TCT TCT TTT TGT TTC TGG CCT GGT G-3' (FRAG. NO:1205) (SEQ. ID NO:1214)
5'-CTC TCT CGT GCC CTT TCC-3' (FRAG. NO:1206) (SEQ. ID NO:1215)
5'-CTT GGG TGT CTT GTT TTT GT-3' (FRAG. NO:1207) (SEQ. ID NO:1216)
5'-GGC CTC CBC CBG GGB CBT G-3' (FRAG. NO:1208) (SEQ. ID NO:1217)
55 5'-CGGBGTGGG GGTCTGGBC GGCCTGGBG GCBTCCBGGG CTCCCTCCB GTCCTTCTTG TCCGCTGCCB
GCBCCCTTC BTTCBGBGG CTBTGGCCT CCBCCBGGG CBTGTTBGG TBGBBCTBG GBGGCC-3' (FRAG.
NO:1793) (SEQ. ID NO: 1806)

Human Cathepsin G Nucleic Acid and Antisense Oligonucleotide Fragments

- CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG GBGBBBGGCC BGCBBBGGCB
 GGBGTGGCTG CBTCTTTCCT GGTGGGGCCT GCTCTCCCGG CCTCCGTGTG TTGCTGGGTG TTTTCCCGTC
 TCTGGTCTGC CTTCGGGGGT CGT-3' (FRAG. NO:1794) (SEQ. ID NO: 1807)
 5'-GBBGBTCGCC-3' (FRAG. NO:1795) (SEQ. ID NO: 1808)
 5'-CBGCCCCBG-3' (FRAG. NO:1796) (SEQ. ID NO: 1809)
 5'-TCC CGT CTC TGG-3' (FRAG. NO:1797) (SEQ. ID NO: 1810)
 5'-GTG GGG CCT GCT CTC CCG GCC TCC G-3' (FRAG. NO:1209) (SEQ. ID NO:1218)
 5'-TGT GTT GCT GG GTG TTT TCC CGT CTC TGG-3' (FRAG. NO:1210) (SEQ. ID NO:1219)
 5'-TCT GCC TTC GGG GGT CGT-3' (FRAG. NO:1211) (SEQ. ID NO:1220)
 10 5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBCT CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG GGBGTGGGGC
 CTGCTCTCCC GGCCTCCGBT GBTCTCCCCT GCCTCBGCCC CBGTGGGTBG GBGBBBGGCC BGCBBBGGCB
 GGBGTGGCTG-3' (FRAG. NO:1798) (SEQ. ID NO: 1811)

Human Defensin 1 Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-CCGGGGCTGC BGCBBCTCB TCBGCTCTTG CCTGGBGTGG CTCBGCTGG GCCTGCBGGG CCBCCBGGBG
 15 BBTGGCBGCB BGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGBTCCTC TBGCTBGGCB GGGTGBCCBG
 BGBGGGC GGG TCC TCB TGG CTG GGG GCC TGG GCC TGC BGG GCC GCT CTT GCC TGG BGT GGC TC GCC CBG
 BGT CTT CCC TGG T GCTCAGCTC CAAAGGAGCC AGCTCTCCC CAGTCTCTGA AATCTGAGT GTTGCTGCC
 AGTCGCCATG AGAACTTCCT ACCTTCTGCT GTTTACTCTC TGCTTACTTT TGTCTGAGAT GGCCTCAGGT
 20 GGTAACCTTC TCACAGGCCT TGGCCACAGA TCTGATCATT ACAATTGCGT CAGCAGTGA GGGCAATGTC
 TCTATTCTGC CTGCCCCATC TTTACCAAAA TTCAAGGCAC CTGTTACAGA GGGAAAGGCCA AGTGCTGCAA
 GTGAGCTGGG AGTGACCAGA AGAAATGACG CAGAAGTGAA ATGAACTTTT TATAAGCATT CTTTAAATAA
 AGGAAATTTG CTTTTGAAGT AT CTGCAGTGGT AAAAAGATTG TATATCTGCT GTTTGATGAA TGCAGCACCC
 ACTAGCCACA TAGTGCTCGT GAGCACTGC AATGCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAACA
 25 GCCACAGGGA GCATGTGGCT GCCATATTGG ATGGTGCTGC TTTGAGAACA AATGAGAGA AATGAAGCCT
 CTATTTACCT TGGTTGGCGG AACACATTGA AGGGACTCTG TATTGATACC AGGCTTCAAA CTTTGGGAAG
 TGTACTGGCC AACTTAAACA CATCCACAGG AGAATGAAGA GGTGTTGGGAA GGGACCAGAA ACCAGGCATT
 GAGGACAATG AGAAGAGTTT TTCAAAAGTG GAATTACTGC AAAAAGTGGA AAAATAGCCT TTGGATGGAA
 GTTACTGATG AGACAATTTT CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT
 30 ACTGTCTCCT AGGGTAGCGA TGGCCTCTTG TATTAAGTCCG CTCAGGCTAC CAGATTTATC GTTTAAACTG
 CCCATAAACA GACCAGGCAG TTAAACAAC AGAAATTTAT TTCTTCGCAG TCCTGGAGGC AGGAAGTCTG
 CGATCAAGGT GGAAGCAGGG TTGGCTTCTT CTCAGGTGTC TGTCTTGGC TGGTAGATGA CCGCCGCCCTC
 CCTGGGTCCT CACATGGTCT TTCCTCTGTG TGTGTCTGTC CCAATCTCTT CTTATAAGGA TGCAAGTCTT
 ATGGATCAGA GCACACCCCA ATGACCGTGT TTAACCTGAA TCACCTCTTT AAAGTTTCTC TCTCAAATA
 CAATCACCTC CTGAGGCACT GTTAGGGCTT CGACACAGGA ATTCTTTTCC TAGGGGATTC AGTTCAGTCC
 35 AAAACGCCTA CCAGTGGAGA CTTGCAACAT GGCGGCCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC
 TGTTCCTGTG TGCATGGAAT AGAAGGCTAT TCCAGAGTAC TGTCTCTATT TATCAGATCT GGGATACTGG
 GAGAAGGGCA AAATAAAGTC CAAGTAGAAA AAAAACTAT GAAAGTTTGA GAGAGTAACC ATAATTTCAG
 CCCGATGTGA AACGATCCTA GATTTCAGT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG GGATTCAAGG
 CAGAGGGAAC AGCGTAACTG AAGGCATGGA AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGCTGC
 40 TTCCACATTT CTAACACACA GGATGTGATT TTGGGTGTG TTGAGACAAG GCAGAAAACCT TGTTTGGAAA
 AATAACTTGA ATTCCCTGCA CATTTAAAT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCATGTTT
 ATTCCTTGGC TTGTATTTGG SCACAGCTGG CATAGCCCCA GACTGAGTAA GCTCTCAGA CACCTCATTT
 CATGAGTAGC CCCAAAGATC AATCATGGGC CAATTTCTTG GAAGAGAAGA CTCTCCGGTG TTTTGCAGTT
 ATTTGTTCTG CTTTCGCGAG ATGTTCTCAA ATCGTTGCAG CTACAAGCCA TGAGTCTGAA GTGTTTGTGT
 45 TCCCTCCTTA CAGGTGGTAA CTTTCTACA GGCCTTGGCC ACAGATCTGA TCATTACAAT TGCGTCAGCA
 GTGGAGGGCA ATGTCTCTAT TCTGCCTGCC CGATCTTAC CAAAATTCAA GGCACCTGTT ACAGAGGGAA
 GGCCAAGTGC TGCAAGTGAG CTGAGAGTGA CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTTATAA
 GCATTCTTTT AATAAAGGAA AATTGCTTTT GAAGTATACC TCCTTTGGGC CAAAATGAAT CTTGTGTCTC
 AATTGGAAGA GGTAAAGAAG TAGGGGGTTA GGGTGCATGG GTTGGAAACGT GAGACAGGTC GAACCAAAA
 50 GCCTGCCTGG AAAAGGGGAG TGACGTCCTA GGCTTCAGTG ATGTCACCTC CACTTTGTTT GATCCACAAA
 CCAACAGGTG ACTGATTTTG GTCAGCTCAG CCTCCAAAGG AGCCAGCCTC TCCCAGTTC CTGAAATCCT
 GAGTGTGCCC TGCCAGTCGC CATGAGAACT TCCTACCTTC TGCTGTTTAC TCTCTGCTTA CTTTGTCTG
 AGATGGCCTC AGGTGGTAAC TTTCTCACAG GCCTTGGCCA CAGATCTGAT CATTACAATT GCGTCAGCAG
 TGGAGGGCAA TGCTCTATT CTGCCTGCCC GATCTTTACC AAAATTCAAG GCACCTGTTA CAGAGGGAAG
 55 GCCAAGTGCT GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT GACGCAGAAG TGAAATGAAC TT -3'
 (FRAG. NO:1799) (SEQ. ID NO: 3010)
 5'-GTCAGCTCAG CCTCCAAAGG AGCCAGCCTC TCCCAGTTC CTGAAATCCT GAGTGTGGCC TGCCAGTCGC
 CATGAGAACT TCCTACCTTC TGCTGTTTAC TCTCTGCTTA CTTTGTCTG AGATGGCCTC AGGTGGTAAC
 TTTCTCACAG GCCTTGGCCA CAGATCTGAT CATTACAATT GCGTCAGCAG TGGAGGGCAA TGTCTCTATT
 60 CTGCCTGCCC GATCTTTACC AAAATTCAAG GCACCTGTTA CAGAGGGAAG GCCAAGTGCT GCAAGTGAGC
 TGGGAGTGAC CAGAAGAAAT GACGCAGAAG TGAAATGAAC TT-3' (FRAG. NO:) (SEQ. ID NO: 2475)

09543679 040400

5'-CTGCAGTGGT AAAAAGATTC TATATCTGCT GTTTGATGAA TGCAGCACCC ACTAGCCACA TAGTGCTCGT
 GAGCACTTGC AATGCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAACA GCCACAGGGA GCATGTGGCT
 GCCATATTGG ATGGTGCTGC TTTGAGAACA AAATGAGAGA AATGAAGCCT CTATTACCT TGGTTGGCGG
 AACACATTGA AGGGACTCTG TATTGATACC AGGCTTCAAA CTTTGGGAAG TGTACTGGCC AACTTAAACA
 5 CATCCACAGG AGAATGAAGA GGTTTGGGAA GGGACCAGAA ACCAGGCATT GAGGACAATG AGAAGAGTTT
 TTCAAAAGTG GAATTACTGC AAAAAGTGGA AAAATAGCCT TTGGATGGAA GTTACTGATG AGACAATTTC
 CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT ACTGTCTCCT AGGGTAGCGA
 TGGCCTCTTG TATTAGTCCG CTCAGGCTAC CAGATTTATC GTTTAAACTG CCCATAAACA GACCAGGCAG
 TTAAACAAC AGAAATTTAT TTCCTCGCAG TCCTGGAGGC AGGAAGTCTG CGATCAAGGT GGAAGCAGGG
 10 TTGGCTTCTT CTCAGGTGTC TGTCTTGGC TGGTAGATGA CCGCCGCCTC CCTGGGTCCT CACATGGTCT
 TTCCTCTGTG TGTGTCTGTC CCAATCTCTT CTTATAAGGA TGCAAGTCTT ATGGATCAGA GCACACCCCA
 ATGACCGTGT TTAACCTGAA TCACCTCTTT AAAGTTTCTC TCTCCAAATA CAATCACCTC CTGAGGCACT
 GTTAGGGCTT CGACACAGGA ATTCTTTTCC TAGGGGATTC AGTTCAGTCC AAAACGCCTA CCAGTGGAGA
 CTTGCAACAT GCGGCCTGC TGGTCCCTCG CCAGGAATAT CACAGGCGAC TGTTCCTGT TGCATGGAAT
 15 AGAAGGCTAT TCCAGAGTAC TGTCTCTATT TATCAGATCT GGGATACTGG GAGAAGGGCA AAATAAAGTC
 CAAGTAGAAA AAAAACTAT GAAAGTTTGA GAGAGTAACC ATAATTTTCA CCCGATGTGA AACGATCCTA
 GATTTACAGT GAAATAGTGA TGTGGGAAGT GAGGGGGCCG GGATTCAAGG CAGAGGGAAC AGCGTAACTG
 AAGGCATGGA AGGAGGGAAG TGTAGGCTGT GTTTGAAGAG TGGCAGCTGC TTCCACATTT CTAACACACA
 GGATGTGATT TTGGGGTGTG TTGAGACAAG GCAGAAAACCT TGTTTGGAAA AATAACTTGA ATTCCCTGCA
 20 CATTTAAAT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCACTGTTT ATTCTTGGC TTGTATTGCG
 SCACAGCTGG CATAGCCCA GACTGAGTAA GCTCTTCAGA CACCTCATTT CATGAGTAGC CCCAAAGATC
 AATCATGGGC CAATTTCTTG GAAGAGAAGA CTCTCCGGTG TTTTGCAGTT ATTTGTTCTG CTTTCGCGAG
 ATGTTCTCAA ATCGTTGCAG CTACAAGCCA TGAGTCTGAA GTGTTTGTGT TCCCTCCTTA CAGGTGGTAA
 CTTTCTCACA GGCCTTGGCC ACAGATCTGA TCATTACAAT TGCCTCAGCA GTGGAGGGCA ATGTCTCTAT
 25 TCTGCCTGCC CGATCTTTAC CAAAATTCAA GGCACCTGTT ACAGAGGGAA GGCCAAGTGC TGCAAGTGAG
 CTGAGAGTGA CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTTATAA GCATTCTTTT AATAAAGGAA
 AATTGCTTTT GAAGTATACC TCCTTTGGGC CAAAATGAAT CTTGTGTCTC AATTGGAAGA GGTAAAGAAG
 TAGGGGGTTA GGGTGCATGG GTTGAACGT GAGACAGGTC GAACCACAAA GCCTGCCTGG AAAAGGGGAG
 TGACGTCCTA GGCTTCAGTG ATGTCACCTC CACTTTGTTT GATCCACAAA CCAACAGGTG ACTGATTTTG-3'
 30 (FRAG.NO:) (SEQ. ID NO: 2474)
 5'-GCTCAGCCTC CAAAGGAGCC AGCCTCTCCC CAGTTCCTGA AATCCTGAGT GTTGCCTGCC AGTCGCCATG
 AGAACTTCTT ACCTTCTGCT GTTTACTCTC TGCTTACTTT TGTCTGAGAT GGCCTCAGGT GGTAACCTTC
 TCACAGGCTT TGGCCACAGA TCTGATCATT ACAATTGCGT CAGCAGTGGA GGGCAATGTC TCTATTCTGC
 CTGCCGATC TTTACCAAAA TTCAAGGCAC CTGTTACAGA GGGAAAGCCA AGTGCTGCAA GTGAGCTGGG
 35 AGTGACCAGA AGAAATGACG CAGAAGTGAA ATGAACCTTT TATAAGCATT CTTTAAATAA AGGAAAATTG
 CTTTGAAGT AT-3' (FRAG.NO:) (SEQ. ID NO: 2472)
 5'-CCGGGGC-3' (FRAG.NO:1800) (SEQ. ID NO: 1813)
 5'-GG GCCTGCBGGG CC-3' (FRAG.NO:1801) (SEQ. ID NO: 1814)
 5'-GGCBGCB BGG-3' (FRAG.NO:1802) (SEQ. ID NO: 1815)
 40 5'-GGG TCC TCB TGG CTG GGG-3' (FRAG. NO:1212) (SEQ. ID NO:1221)
 5'-GCC TGG GCC TGC BGG GCC-3' (FRAG. NO:1213) (SEQ. ID NO:1222)
 5'-GCT CTT GCC TGG BGT GGC TC-3' (FRAG. NO:1214) (SEQ. ID NO:1223)
 5'-GCC CBG BGT CTT CCC TGG T-3' (FRAG. NO:1215) (SEQ. ID NO:1224)
 5'-CCGGGGCTGC BGCBBCTCB TCBGCTCTTG CCTGGBTGG CTCBGCCTGG GCCTGCBGGG CCBCCBGGBG
 45 BBTGGCBGCB BGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGTCCTC TBGCTBGGCB GGGTGBCCBG
 BGBGGGC-3' (FRAG.NO:1803) (SEQ. ID NO: 1816)

AGGTTCTTCA GAACCTGACA TTTTAAATGA AGAGGTCAGG CAGTTCATGA GGAAAGCCTC ATTGTCCCCA
 TGTCTCTGTC ACTGCTGCAC CCCTGAGACA TCACAGACAT GGACACTGGG GCCTGCTTGT TTCTCAAACT
 GCCCTTAGAT CGAAAGAGGG AGGAACCAGG ATGAATGCCA CTCATTTTCC CAAGAAAGGC CCTCTCCTGA
 GTGCCCCGGA TGGGGCTCTG TCCATTGCCT GGGGCCGCCA ATTGCTACTC TGGGTTACGG AGGAAGGACA
 5 GGGTCCTGAG AGACACCAGA GACCTCACAC AGCCCTGAAA ACATGGGGCT CCTTCATAAG TGTTCCTCAT
 CACCAACAGG GAGACCACGT GGAGGCCTTG CAGCCCCACT CGGTGCTTCT CCACCAAATC CCAAGGGCAG
 TGACGCTGAC GTCTGTGGAA AGCAGAGAAA GCCCTGGCTC CCAAAGCCCT GAAGTCCCTG TGGAGCTGAC
 ATTCCTTGAG TGACGGTGTG AATGGAAGGA ACTCAAGTGC GGGTGGTAGG CCACCTCCTG GCCCAGGCCCT
 GGGTGAATC TGAGGGGACA CATGTAGTCA CAATCCCATC CTCCCATTCT CCTTCTCAGA GGAAGGAAGT
 10 GGGCATCCAT CTGCCTCATC TCTCTCCCGT GGGGAAGATG GGGAGTTTCA GGGGAACCTT CACTAAATAT
 TCACCAGCTC AGATCTCCTG TGAGGATGGG GCCCACCATG CTCCCGGTGC TGCCAGAGGC CCTGAGCCCC
 TCCCAGGGTC CCTGGGTTTG AGCCAGCCCT GTATCATCCC CAGGAGCTGA ATGTCAGAGC AATGGATAGA
 ATTAGATGGA AAGAGCTCTC AATTTGACCT GAGACTGTCC CCAGATACTC AGGAAAAACA GGACGTCGCA
 CAGAGTGGGC AGCAGGTGAG TGGCAGGTTA TAGGTCCTGA GTTTGAGTTT GTTCTCACGT GAGACAGACC
 15 CAGCCCCTCA CTCCATTAC ACCTGGGTT TAAATGGTG CAAGATAGGA GCAATTTTCT GGTCCCAAGA
 GCAGGAGGAA GGGATTTTCT GGGGTTTCT GAGTCCAGAT TTGCATAAGA TCTCCTGAGT GTGCATTGTT
 CTTTGAGGAC CATTCTCTGA CTCACCAGT AAGTGGCTGA ATTCTAACCT CTGTAATGAG CATTGCACCC
 AATACCAGTT CTGAACTCTA CCTGGTGACC AGGGACCAGG ACCTTTATAA GGTGGAAGGC TTGATGTCTT
 CCCCAGACTC AGCTCCTGGT GAAGCTCCCA GCCATCAGCC ATGAGGGTCT TGTATCTCCT CTCTCGTTC
 20 CTCTTCATAT TCCTGATGCC TCTTCCAGGT GAGATGGGCC AGGGAAATAG GAGGGTTGGC CAAATGGAAG
 AATGGCGTAG AAGTTCTCTG TCTCTCTCA TTCCCTCCA CCTATCTCTC CCTCATCCCT CTCTCTCCTT
 CCTCTCTCTG TGTGTCCCTT CCATCCTTTT CTCCTGCTTC TCTCTCTCTC TCCCTCTCTC TCTTTTTTCT
 GTCTTTCTTT TTCTCTCTC CCTAGAGCAT GTCTTTCTTT CTTTCTCTTT CCTTCTCTT ACCCACACTT
 25 TTAGACTGAA TGCCCTATTT AATTGAACAA AGCATTGCTT CCTTCAATAG AAAAGGAGTT TGAGAACCCA
 ATGGACACCT CACTCGTTCT TCTAAGCCAA TATGAAGGAG CCCAGTAGCT TGTAATATC ATCTCTTCAC
 TGCTTTCCAT GCTACAACTG CTGAGACTAT GGTGAAACC TTTTAGGTGA CTTTTTAAAT AAAAGGCAGA
 AATTTTGATT TTATCTAAAG AAAGTAGTAT AGAATGTCAT TTTCTAAATT TTTATATTTA AAGGGTAGAT
 ACTGCAACCT AGAGAATTCC AGATAATCTT AAGGCCCAGC CTATACTGTG AGAACTACTG CAGCAAGACA
 CTCTGCCTCC AGGACTTTTC TGATCAGAGG CCCTGAGAAC AGTCCCTGCC ACTAGGCCAC TGCAGGTTCA
 30 CAGGACAGGG TACAGCCCAT TGAAACCTAC TTTTAAACCT GGATGCCTAA CCTTCATTTT CTCCTTGATA
 TTATGAAAAT AAAATAAAAA CCATGAAAGG ATAAAAGAGG GAGAGTGGA GGGAAAGGATG GAGAAAGGGA
 AAAAGAAAAT TTGAGAGTAA ATCCTAAAAAC AATTAATCTA ATAGATATCA TCTTGTGAAA TCCTCATTTT
 ACCAATCTTA TTTATGAGT CTGGGTTTTG TGAGAACAA GGGGTCTGA GAGGCACCAG AGACCTCATG
 35 TTTTCCAAAA CCTAGAACAG TATAATGAAG GAAGCGGGG AGGCAGGGAG GCAGGGAGGC AGGGAGGCAG
 GGAGGCGGGC AGGTGGGGAG GGAGGGACGG AAGGAGGGAG GGAGGGAGGG AGGGAGGGAG GGAGGGATAA
 AAAAAGAAGA ATGAGGTTGA AACCAGGACT TAGATATTAG AAACAAGCCA TTACAAAATT TATTCTATG
 GTTAATTGTG GTTTTCAACT GTAAGTTACT TGGTGTTAAT TTCCTATTAA ACAATTTTCT TAAGTTGCAT
 CTTTTTATCC CATCTCAGGT CAAATACTTA ACAGACTAAA TGATTTGAAA AAGCAAAAGT TTAGTGCTT
 GTGTGTGTTA AAATGGAGGT ATGGTGGCTT TGATATTATC TTCTTGTGGT GGAGCTGAAT TCACAAGAGA
 40 TCGTTGCTGA GCTCCTACCA GACCCACCT GGAGGCCCCA GTCCTCAGG AGAGATCAGG GTCTTTCACA
 ATCAGGTTCT AAAAAATAA ACATCCCCC AACCACAGCA GTGCCAGTTT CCATGTCAGA AACTTAGATC
 CAAATGACTG ACTCGCTCT CATTATCAT ATGAAAAAG CCAGGCTTGA GAAAGAAGCC CGCTGCGGAT
 TTAGTCAAGG CGATACTGAC ACAGGGTTTG TGTTTTCCA ACATGAGTTT TGAGTTCTTA CAGCTGTTT
 GCTCTTTTTG TGTGTTTTTT CCCTGTTAGG TGTTTTGGT GGTATAGGCG ATCCTGTTAC CTCCTTAAAG
 45 AGTGGAGCCA TATGTCATCC AGTCTTTTGC CCTAGAAGGT ATAAACAAAT TGGCACCTGT GGTCTCCCTG
 GAACAAAATG CTGCAAAAAG CCATGAGGAG GCCAAGAAGC TGCTGTGGCT GATGCGGATT CAGAAAGGGC
 TCCCTCATCA GAGACGTGCG ACATGTAAAC CAAATTAAC TATGGTGTCC AAAGATACGC AATCTTTATC
 CTAGTAATTG TGGTCATTGG GTGATGTTGG TTTGGGCAGG CCATCTCTAA TATCCTTGAA ACACCTTTTT
 CTGCTCTCCA GGAAGGGGTC AGGGCTGCCA CAGCGGGGCT TGGAGTGCTT TCCAGGGTCA CAGGCATCTG
 50 TATTCTTTGG ATTCCTTGAC CTTCCTTAC ATTTCCCGC ATTTCCTAA AACGTGTGCT TTGCTCCTCC
 TGCATCCTCC CCTTGCATGC CCTCACCTAC CCCACACTCT CCCTAAAAAA AGCAAGCCCA ACTCAAAGAC
 CAGTTCCTTC ATGGAATCAT AGTGGATCTG CCAAGGGAGG GGATGCCCAG TCCTCTGTTT TTCACAGAC
 TCCCTTCTTC TGCTAAGGT TTCTTATGCA ATTAT GAATTCACAT TTCTCACCTT TTGATGTATT AAGAAAGTAT
 GGAGAAATAT ATCCTCTATC AAATTTTCAT GCCTTCAATA ATTTCTAATT CATCAGTCAG TGTTTTTCCA
 55 TCCTTTACTG TGATGATGCC CTTTCTTCCA AACTTTTTC TGGCATCAGA GATGATGTTA CCAATTTCTT
 TGTCTCCATT TGCAGAAATT GTAGCAACCT GTGCAATTTC TTCAGGTTTG GTCACAGGTT TAGACTGCTT
 TTTAAGTTCA GCAATTACAG CATCAACAGC TAACATCACA CCTCTCTTGA TTTCCACTGG ATTAGCACCT
 TTGCTAACCT TCTGGAAGGC TTATTTGGAA ATAGAGCATA CCAGTACAGC AGCAGTGATA GTGCCATCCC
 CCAGTCTCTC CATTGTGTT ATTGGCAACA TCTTGGACAA GTTTAGCTCC AATGCTTTTA TATTTATCCT
 60 TTAAGTCAAT TGACTTTGCA TCAGTCACAC CATCTTTTGT TACTTTGGGA CTTCCCAGC TATGTTCAT
 AATTACTGTT CTTCCCTTTG GCCCCATTGT AATGGCTACA GCATCGACAA AAAGTCTACA CTTTGAAGCA
 TTAAGGCTCA GACATCAGCA CCAAATTTTA CATCTTTACC ATCACTTCAA GTGAGGTGAG GAGCCAGTAG

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CCTGGACACT GGTCTCATCT GGTGAAAGAC TGTGGGTAAT GGAAGCATT CTGTGGGGTG GTGGCAGGAC
 ATGTGCATGG TGAGGCAGGT CATCAGCAGC AAGTGAGAGC TGCCTCTTAC TTCTAAAGG TGACATAGCA
 AGTATACAAA AAAAAATAAA ATATTAATTT AGGCAGAGCA CATAAAGGCT TTATTTTATA TTCCATTTCT
 CTGTATGCTT TCTTCACCAG GAAGAAATAG TTTTAGTGTC AGGAATGAAT GAGTCTGCCC CTCAATTCCA
 5 GCCTGCTCAG CACACAAGGA AACAAAGCCC TGACAATCAG AGTGACTCCC TGGTGACTAA GCTCCAGTCC
 TGGATGCATA TTTGTTTAGC AGTTCTGACA GCATCTGACC CAGCCCTCTC TTTGCATACC CCACCAGAAC
 CTCTCTTTT TTTTTTTTCT TTTGAGACTG AGTCTTGCTC TGTGCGAAGC GATTCCCGTG CCTCAGCCTC
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 AGTGATGAG GTTGCTGCAG CCCCGAGCA GATTGCAGCG GACATCCCAG AAGTGGTTGT TTCCCTTGCA
 50 TGGGACGAAA GCTTGGCTCC AAAGCATCCA GCTGAGAGAG GCAGGCATGC AGAGCTGCTA AGTCTAGAGG
 GAAGGACGGG AGAGAGGTTT CAGAGTTGGG TCTCAGAGT CTATGTCACT GAGGTGGCTT CACTTAGAAT
 CTCTGGGCAT TGATTTTCTC ATCTAGAAAT TGAACAGAGA GCTGAGATAA CCGTGAAGAAC TTTATTCTC
 CAAAGACTTG ATTCCAAGAA ACATCTGTGA AATTCACTAA GTTAAAGATA TGAAGAGACA GACTAGTTAT
 TTCTGGATCT AAACAAGTAG ACTTAGTTGT AAAGAGAACA TTTTACTCTA TCTACAGAAG AGCTTTTAAA
 55 AACTGCAGCC AAGCCTGAGG GTAAGTTCAG GTGTGTGTGT GATGGGGCAG GAATGCAAAA ATGAGAGCAA
 AGGAGAATGA GTCTCAAATT CTGTGTGACA AGCACTGCTC TGCGTGTTA TCCTATCGA CTGAGGTGTG
 TCGTGCTACC GGCTGCAATG CAGCCAGCAT CACCTGTCAG CTAGCATGTG ACTTCCCCGA GATTCTTTTT
 CTTACCCACT GCTAACTCCA TACTCAATTT CTATGCTCT CCCTGTCCCA GGCTCAAGGA AAAACATGGA
 CTGCTATTGC AGAATACCAG CGTGCAATG AGGAGAACCT CGCTATGGAA CCTGCATCTA CCAGGGAAGA
 60 CTCTGGGCAT TCTGTGCTG AGCTTGACGA AAAAGAAAAA TGAGCTCAAA ATTTGCTTTG AGAGCTACAG
 GGAATTGCTA TTAATCTGT ACCTTCTGCT CAATTTCTCT TCCTCATCTC AAATAAATGC CTTGTACAA
 GATTTCTGTG TTTCCACCTC TTTAATGTGT GATATGTGTC TGTGTCAAGA CACTTGGGAT ACACGTACCA

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 0543679 040400

AAACGCAAAA TCAAATTTTT GAACAATATA-3' (FRAG. NO:) (SEQ. ID NO:3012)

Human Defensin 3 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTCBGCTC TTGCTTGGBTG GCTCBGCTGG GCCTGCBGGG
CCBCCBGBGB BTGGCBGCBG GBTGGCBGGG TCCTCBTGGC TGGGGTCBCCT GGBGBGGGB GBGCBGGGG
5 TCCTCBTGGC TGGGGTCCCT CTCTCCCGTC CT CCTACCTTGC TATAGAAGAC CTGGGACAGA GGACTGCTGT
CTGCCCTCTC TGGTCACCT GCCTAGCTAG AGGATCTGTG ACCCAGCCA TGAGGACCCT CGCCATCCTT
GCTGCCATTC TCCTGGTGGC CCTGCAGGCC CAGGCTGAGC CACTCCAGGC AAGAGCTGAT GAGGTTGCTG
CAGCCCCGGA GCAGATTGCA GCGGACATCC CAGAAGTGGT TGTTCCTT GCATGGGACG AAAGCTTGGC
TCCAAAGCAT CCAGGCTCAA GGA AAAACAT GGACTGCTAT TGCAGAATAC CAGCGTGCAT TGCAGGAGAA
10 CGTCGCTATG GAACCTGCAT CTACCAGGA AGACTCTGGG CATTCTGCTG CTGAGCTTGC AGAAAAAGAA
AAATGAGCTC AAAATTTGCT TTGAGAGCTA CAGGAATTG CTATTACTCC TGTACCTTCT GCTCAATTTC CTTT-3'
(FRAG. NO:1804) (SEQ. ID NO:3013)

5'-CCTACCTTGC TATAGAAGAC CTGGGACAGA GGACTGCTGT CTGCCCTCTC TGGTCACCT GCCTAGCTAG
AGGATCTGTG ACCCAGCCA TGAGGACCCT CGCCATCCTT GCTGCCATTC TCCTGGTGGC CTGTCAGGCC
15 CAGGCTGAGC CACTCCAGGC AAGAGCTGAT GAGGTTGCTG CAGCCCCGGA GCAGATTGCA GCGGACATCC
CAGAAGTGGT TGTTCCTT GCATGGGACG AAAGCTTGGC TCCAAAGCAT CCAGGCTCAA GGA AAAACAT
GGACTGCTAT TGCAGAATAC CAGCGTGCAT TGCAGGAGAA CGTCGCTATG GAACCTGCAT CTACCAGGA
AGACTCTGGG CATTCTGCTG CTGAGCTTGC AGAAAAAGAA AAATGAGCTC AAAATTTGCT TTGAGAGCTA
CAGGAATTG CTATTACTCC TGTACCTTCT GCTCAATTTC CTTT-3' (FRAG. NO:) (SEQ. ID NO:2478)

5'-GAATTCCTG TAAGCCCTGT TACAGGGGCT GCACCCAGA TACAACCTGA CCTGTGTCCA AGGCGGGCAA
20 CTCAACCTT AGATATTGAA TGGGTCCCAT GGCACCAATG CTTAAACACC AGCAGCCCTC ACAACCACAG
ATCGTGT TTTT AAGGATGAGG AGGTAGTTCT CTGGATGCAC AGGCTTCAAT CCAAATGGGC TCATGACGCC
GCAGCACACA CCCAGTCTGC AGCCTGAAGA GTTGGAGCAT TGCATTACAA GAAAGCATCC AGACATGATC
ATGGGCTCAG GGATACACCT GTTCTCCGAT GTGTACCAGT GAAGGATGGA AACTCTATG CCTCCAGAA
25 AGCACCCTC AAGCTTTTGC TGAATGCTTC TCTGAAGGCC CACAAGGCTG AGAGGCTGTG CAACACCAGC
AGTAAAGTGA ATGCCAGAC TCCACCTCC TTTCTTGGT GGCCATCTGG AAAGGCCACT CCCACCCTGA
TGGCTAATGC CTCAGACCAG TTCTTGGCCC AGATGATCCT AGACAATTGT TTAAGCTTAA ACTGTTTATT
GGCCAAGCAA ACAGGTGATA GTACCTCTGG GGAACCACAT GCCGCGTGA CATCCAGATC TCAGGAGAAC
CCAAAAATGT CTGTTCCACA TAGCAACAGA AGCCAGGTA GCACTCAGTC TCACCTGGGT GTTCTCCAAC
30 ATCCAGCTC AGCCAAATGG CTTTCATTAG TTTTATGGT TAGACCCAG GTCTCGGGA CACTGCTTTA
GAAACACATT CCAAATCCTC CTCTGTGTGC AGGTGGCATT CCTATCCCA TCTCTTGTCA GGGCGTATAC
TGTGATACGC AGCCAGGCTG TCCAGAGGC CTTAAATATT CCCTTGGTGC AGGTAGTTCA GCTTAGCCAC
AGCCAATGCA TCACAGGGTC AACTGTGTTA GGAGCCATTG AGAATCCATA GTTGGTTGCT GCCTGGGCCT
GGCCAGGGCT GACCAAGGTA GATGAGAGGT TCCTCTGTGG AGTTCTACTT TAACCTCACC TCCCACCAA
35 ATTTCTCAAC TGTCTTGCC ACCACAATTA TTTAATGGAC CCAACAGAAA GTAACCCCGG AAATTAGGAC
ACCTCATCCC AAAAGACCTT TAAATAGGGG AAGTCCACTT GTGCACGGCT GCTCCTTGCT ATAGAAGACC
TGGGACAGAG GACTGCTGTC TGCCCTCTCT GGTCACCTG CCTAGCTAGA GGATCTGTAA GTACTACAAA
ACTTAAACTT TACACTGAGT TTTTCATT GAAGCTATGC CTCCAATCTG ACCTCTGACT GTGGGGCCGC
CCCAGAGGGA CCCAGCGGGT GAATCCCTGC TAGGAACGTC TGTCGGGACC TCTGGTGACT GCTGGGGACG
40 ATGGCTTCCA GCTAACTTAA TAGAGAACT CAAGCAGTTT CCTTCTAAAT ACACATGTCA CATGTCCTGG
TTGACATGTC CAGTAAGAAG ACTATCACAG GTCTTTGGAA CATTCTTTG AGAGAAACCT ATTTAGGTCC
TTGGTCTGTT TTTCAATCAG GTTGTGTTGAT TTTTGTCTT GAGTTGTTG AATTCCTTAT GTATTAGAT
ATTTGCCCT TCTGCCATGT AGGTGTTGCA AATTTTCT CTATTTTCT GGGTTATCTT TTTCTCGGT
TGATTGTTTC CTTTGTGTG CAGATGCTTT AGCGTTAAAT GAAGCCACAC TTGTCTATTT TCCCTTTTAT
45 TGCCTGTGCC TTTGGTGTCA TAGCCAAGAA ATCATTACCT ACATCAATGT CAAAAGCTTT ATCTTCTAT
ACACTTCTAG TAGTTTATGG TTTTCAAGT TACATTAGG TTTTCAATC ATTCTGAGTT ATGTTCTCTA
CATGGTGTGA GATAAAGATT TAAATACATA CATATATAAA ATCATGAGGT AGTGTAACAT ATAAATATAC
AATTGTTAAT TGTTACTCAA GTCTAAGTAG AGGTGGAAAT AATAAACTTT CTTTTTTTTA CTTAAACCAC
TCTGTGTCAC TGAGCTGATT TCACCTTTAG CCTGATAAAA TCATTGTCCT CTCCACCCTG ATTCCTACAG
50 GAGACTACTC ACCCATAAC CTCAAAAACC TCTTCATGAG GATGGTAAGT CACCTGAATC CTGAAGTGAA
TTACTCGCTA TTCCATTGGA ACTCATATAG GACACCAGAA TCTAGACCTC CAGAGAACAG CAGGACCCAT
CTTCAGAAAA TAAGAAGCAT TTGTTCCCTG AGCCTGTTGA ATCAAAGTGC AATTTCTATT CTTTTTGGAA
TGTTAAAAAG TGAATCATAA TATTTAAGCA GGTGAACCCA CGAGTAACAT AGCAGGGTCT TTCTTGTCT
TATTAGCTCC AACCTAGCAC AGACATTAAA GGTACAGATG TATACTAGCA TGAACTGGG AGAACAGGAG
55 CATTCGAGCA ACCTTGAGAC CAATGGGCCT CTCTTATAAA ATGCACACCT CCTCTCACTG AGATTGAGGA
AGGTTTCTTG TCTCCGAGCC TTCTCCAGT AGAGCTATAA ATCCAGGCTG GTCCTCCCT CCCCACACAG
CTGCTCCTGC TCTCCCTCCT CCAGGTGACC CCAGCCATGA GGACCCTCG CATCCTTGCT GCCATTCTCC
TGGTGCCCT GCAGGCCAG GCTGAGCCAC TCCAGGCAAG AGCTGATGAG GTTGCTGCAG CCCCAGGACA
GATTGCAGCG GACATCCAG AAGTGGTTGT TTCCCTTGCA TGGGACGAAA GCTTGGCTCC AAAGCATCCA
60 GGTGAGAGAG GCAGGCATGC AGAGCTGCTA AGTCTAGAGG GAAGGACGGG AGAGAGGTT CAGAGTTGGG

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- TCTCAGCAGT CTATGTCAC T GAGGTGGCTT CACTTAGAAT CTCTGGGCAT TGATTTTCTC ATCTAGAAAT
 TGAACAGAGA GCCAAATAAA CCTGAGAAAC TTTATTTCTC CAAAGACTTG ATTCCAAGAA ACATCTGTGA
 AATTCATAA GTTTAAGATA TGAAGAGACA GACTAGTTAT TTCTGGATCT AAACAAGTAG ACTTAGTTGT
 AAAGAGAACA TTTTACTCTA TCTACAGAAG AGCTTTTAAA AACTGCAGCC AAGCCTGAGG GTAAGTTCAG
 5 GTGTGTGTGT GATGGGGCAG GAATGCAAAA ATGAGAGCAA AGGAGAATGA GTCTCAAATT CTGTGTGACA
 AGCACTGCTC TGCCTGTTTA TTCCTATCGA CTGAGGTTGT TCGTGCTACC GGCTGCAATG CAGCCAGCAT
 CACCTGTGAG CTAGCATGTG ACTTCCCCGA GATTCTTTT CTTACCCACT GCTAACTCCA TACTCAATTT
 CTCATGCTCT CCCTGTCCA GGTCAAGGA AAAACATGGA CTGCTATTGC AGAATACCAG CGTGCAATTGC
 AGGAGAACGT CGCTATGGA CCTGCATCTA CCAGGGAAGA CTCTGGGCAT TCTGCTGCTG AGCTTGCAGA
 10 AAAAGAAAAA TGAGCTCAAA ATTTGCTTTG AGAGCTACAG GGAATTGCTA TTAATCTCTG ACCTTCTGCT
 CAATTTCTT TCCTCATCTC AAATAAATGC CTGTGTACAA GATTTCTGTG TTTCCACCTC TTTAATGTGT
 GATATGTGTC TGTGTCAAGA CACTGGGAT ACACGTACCA AAACGCAAAA TCAAATTTT GAACAATATA-3'
 (FRAG. NO:) (SEQ. ID NO:2477)
 5'-GGCBGCBGG-3' (FRAG. NO:1805) (SEQ. ID NO:1818)
 15 5'-GG CTG GGG-3' (FRAG. NO:1806) (SEQ. ID NO:1819)
 5'-GGGGTCBCC-3' (FRAG. NO:1807) (SEQ. ID NO:1820)
 5'-GGG TCC TCB TGG CTG GGG TC-3' (FRAG. NO:1216) (SEQ. ID NO:1225)
 5'-CCT CTC TCC CGT CCT-3' (FRAG. NO:1217) (SEQ. ID NO:1226)
 5'-CGCTGCBBTC TGCTCCGGGG CTGCBGCBBC CTCBTBCTC TTGCTGGBGTG GCTCBGCCTGG GCCTGCBGGG
 20 CCBCCBGGGB BTGGCBGCBG GBTGGCBGGG TCCTBTGTC TGGGGTCBCT GGBGBGGGB GBGCBGG-3'
 (FRAG. NO:1808) (SEQ. ID NO:1821)

Human Macrophage Inflammatory Protein-1-alpha/RANTES Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

- 5'-GTCTTTGTTT CTGGGCTCGT GCCCBTCCC GGCTTCTCTC TGGTTCCGTC CTCTGTGGTG TTTGGCCCTG
 25 CTTCCTTTTG CCTGTTGAGG GGGCAGCAGT TGGGCCCAA AGGCCCTCTC GTTCACCTTC TGGCAGGAGTT
 GCATCCCCATA GTCAAACCTCT GTGGTCGTGT CATAGTCCTC TGTGGTGTTT GGAGTTTCCA TCCCGGCTC
 TCTCTGGTTC CAAGGGAGB GGGGCBGCB GTTGGGCCB BBBGGCCCTC TCGTTBCCT TCTGGCBGCG
 BGTTCBCTCC CCBTBGTCBB BCTCTGTTG CTGTCTBTG TCCTCTGTG TGTGGBGT TTCCBTCCCG
 GCTTCTCTCT GTTCCBBGG GB-3' (FRAG. NO:1809) (SEQ. ID NO:1822)
 30 5'-GGGCC CC-3' (FRAG. NO:1810) (SEQ. ID NO:1823)
 5'-GGGGCBGC-3' (FRAG. NO:1811) (SEQ. ID NO:1824)
 5'-CCCGGCTTC-3' (FRAG. NO:1812) (SEQ. ID NO:1825)
 5'-GTC TTT GTT TCT GGG CTC GTG CC-3' (FRAG. NO:1218) (SEQ. ID NO:1227)
 5'-CCB TCC CGG CTT CTC TCT GGT TCC-3' (FRAG. NO:1219) (SEQ. ID NO:1228)
 35 5'-GTC CTCTGT GGT GTT TGG-3' (FRAG. NO:1220) (SEQ. ID NO:1229)
 5'-CCC TGC TTC CTT TTG CCT GTT-3' (FRAG. NO:1221) (SEQ. ID NO:1230)
 5'-GAGGGGGCAG CAGTTGGGCC CCAAAGGCC TCTCGTTCAC CTTCTGGCAC GGAGTTGCAT CCCCATAGTC
 AAACCTCTGTG GTCGT-3' (FRAG. NO:1222) (SEQ. ID NO:1231)
 5'-GTCATAGTCTCTGTGGTGTGAGTTCCATCCCGGCTCTCTCTGTTCCAAGGGA-3' (FRAG. NO:1223) (SEQ. ID
 40 NO:1232)
 5'-GBGGGGGCBG CBGTTGGGCC CBBBGGGCC TCTCGTTCBC CTTCTGGCBC GGBGTTGCBT CCCCBTBTG
 BBBCTCTGTG GTCGTG-3' (FRAG. NO:1224) (SEQ. ID NO:1233)
 5'-TCBTGTCCTCTGTGGTGTGGBGTTCCBTCCCGGCTCTCTCTGTTCCBBGGGB-3' (FRAG. NO:1225) (SEQ. ID
 NO:1234)
 45 **RANTES Antisense Oligonucleotide Fragments**
 5'-GGGCBGCGGG CBGTGGGCG GCBTGTBGG CBBBGCBCB GGGTGTGGTG TCCBGGBBT BTGGGBGGC
 BGBTGCBGB GCGCBGBGG CBGTBGCBBT GBGGBTGBCB GCGBGGCGTG CCGCGGBGC CTTCTGTTB
 CCTGTGGBGB GGCTGTCGGB GGGGTGTGG TGTCCGCTT GCGGTTCTT CCGGTGTTT TTTCTGTTG
 TGGCCTGCTG CTCGTCGTGT CGTCCGCTC CCGGTTCTG CTCGCTCTG CGCCCTTCC TTCCTTGTG
 50 TGTTCCTCCC TTCCTTGCCT CT-3' (FRAG. NO: 1813) (SEQ. ID NO: 1826)
 5'-GGGTTGGC-3' (FRAG. NO: 1814) (SEQ. ID NO: 1827)
 5'-CGGG CBG-3' (FRAG. NO: 1815) (SEQ. ID NO: 1828)
 5'-CCCGGGTTCG-3' (FRAG. NO: 1816) (SEQ. ID NO: 1829)
 5'-GGGTGTGGT-3' (FRAG. NO: 1817) (SEQ. ID NO: 1830)
 55 5'-GGGCBGCGGG CBGTGGGCG GCBTGTBGG CBBBGCBCB GGGTGTGGTG TCCBGGBBT BTGGGBGGC
 BGBTGCBGB GCGC-3' (FRAG. NO:1226) (SEQ. ID NO:1235)
 5'-BGBGGGCBGTB GCBTGBGB TGBCBGCB GCGTGCCGGB GBBCCTTCB TGGTBCCTGT GGBGBGGCTG
 TCGGBGG-3' (FRAG. NO:1227) (SEQ. ID NO:1236)
 5'-GGGTGTGGTGTCCGCTTGGCGGTTCTTTCGGGTGTTCTTCTCTGGGTGGCCTGCTGCTCGTGTGTC-3' (FRAG.
 60 NO:1228) (SEQ. ID NO:1237)

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5'-GCTCCGCTCCCGGGTTCGTCTCGCTCTGTGCGCCCTTCCTTCTTGTCGTGTTCCCTCCCTTCCTTGCTCT-3' (FRAG. NO:1229) (SEQ. ID NO:1238)

5'-GGGTGTGGTGTCCG-3' (FRAG. NO:1230) (SEQ. ID NO:1239)

5'-CTTGGCGGTTCTTTCGGGTG-3' (FRAG. NO:1231) (SEQ. ID NO:1240)

5 5'-TTTCTTCTCTGGGTGGC-3' (FRAG. NO:1232) (SEQ. ID NO:1241)

5'-CTGCTGCTCGTCGTGGTC-3' (FRAG. NO:1233) (SEQ. ID NO:1242)

5'-GCTCCGCTCCCGGGTTC-3' (FRAG. NO:1234) (SEQ. ID NO:1243)

5'-GTCTCGCTCTGTGCGCC-3' (FRAG. NO:1235) (SEQ. ID NO:1244)

5'-CTTCTTCTTGTC-3' (FRAG. NO:1236) (SEQ. ID NO:1245)

10 5'-GTGTTCTCCCTTCCTTGCTCT-3' (FRAG. NO:1237) (SEQ. ID NO:1246)

5'-GGGCBGCGGG CBGTGGGCGG GCBTGTBGG CBBBGBGCB GGGTGTGGT TCCBGGBBT BTGGGGBGGC
BGBTGCBGG BGCGBGBGG CBGTBGBBT GBGGTGBCB GCGBGGCGTG CCGCGGBGBC CTTCBTGGTB
CCTGTGBGB GGCTGTGGB GG-3' (FRAG. NO:1818) (SEQ. ID NO:1831)

Human Muscarinic Acetylcholine Receptor HM1* Nucleic Acid and Antisense Oligonucleotide Fragments

15 5'-GCTGCCCGGC GGGGTGTGCG CTGCGCTC CCGTGCTCG TTCTCTGTCT CCCGGTCCCC CTGCTGGC
GTCTCGGGC TTCGTCTCT TCCTTCTT CTTCCGCTC CGTGGGGGCT GCTTGGTGGG GGCCTGTGCT
CGGGGTCCCG GGGCTTCTGG CCCTGCCGT TCATGGTGGC TAGGTGGGGC GTTCBTGGT GCTBGGTGG GC-
3'(FRAG. NO:1819)(SEQ. ID NO: 1832)

5'-GGTGGGGC-3' (FRAG. NO:1820) (SEQ. ID NO: 1833)

20 5'-GCCCGCGGGG-3' (FRAG. NO:1821) (SEQ. ID NO: 1834)

5'-CGG GGC TTC TGG CCC-3' (FRAG. NO:1822) (SEQ. ID NO: 1835)

5'-GTT CBT GGT GGC TBG GTG GGC C-3' (FRAG. NO:1238) (SEQ. ID NO:1247)

5'-GCT GCC CGG CGG GGT GTG CGC TTG GC-3' (FRAG. NO:1239) (SEQ. ID NO:1248)

5'-GCT CCC GTG CTC GGT TCT CTG TCT CCC GGT-3' (FRAG. NO:1240) (SEQ. ID NO:1249)

25 5'-CCC CCT TTG CCT GGC GTC TCG G-3' (FRAG. NO:1241) (SEQ. ID NO:1250)

5'-GCC TTC GTC CTC TTC CTC TTC CTT CC-3' (FRAG. NO:1242) (SEQ. ID NO:1251)

5'-GCT CCG TGG GGG CTG CTT GGT GGG GGC CTG TGC CTC GGG GTC C-3' (FRAG. NO:1243) (SEQ. ID NO:1252)

5'-CGG GGC TTC TGG CCC TTG CC-3' (FRAG. NO:1244) (SEQ. ID NO:1253)

5'-GTT CAT GGT GGC TAG GTG GGC C-3' (FRAG. NO: 1245) (SEQ. ID NO:1254)

30 **Human Muscarinic Acetylcholine Receptor HM3* Nucleic Acid and Antisense Oligonucleotide Fragments**

5'-GGG GTG GGT BGG CCG TGT CTG GGGGT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT
TGG CTT TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG
GGG GCT TCT TGGCG CTG GCG GGG GGG CCT CTTGCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG
TGGTGG CGG GCG TGG TGG CCT CTG TGGGGG CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCTT TGC
35 GCT CCC GGG CCG CCGG GTG GGT AGG CCG TGT CTG GGGGT GGC CAT GTT GGT TGC CGGG CCC GCG GCT
GCA GGG G-3' (FRAG. NO:1823) (SEQ. ID NO:1836)

5'-CCC GGG CGG-3' (FRAG. NO:1824) (SEQ. ID NO:1837)

5'-G GCG GGG GGG CC-3' (FRAG. NO:1825) (SEQ. ID NO:1838)

5'-CCC GGG CCG CC-3' (FRAG. NO: 1826) (SEQ. ID NO: 1839)

40 5'-GG CCG TGT-3' (FRAG. NO:1827) (SEQ. ID NO:1840)

5'-GGG GTG GGT BGG CCG TGT CTG GGG-3' (FRAG. NO:1246) (SEQ. ID NO:1255)

5'-GTT GGC CBT GTT GGT TGC C-3' (FRAG. NO:1247) (SEQ. ID NO:1256)

5'-TCT TGG TGG TGC GCC GGG C-3' (FRAG. NO:1248) (SEQ. ID NO:1257)

45 5'-GCG TCT TGG CTT TCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GG-3'(FRAG.NO:1249)(SEQ.ID
NO:1258)

5'-GCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT TG-3' (FRAG. NO:1250) (SEQ.ID NO:1259)

5'-GCG CTG GCG GGG GGG CCT CCT CC-3' (FRAG. NO:1251) (SEQ. ID NO:1260)

5'-GCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGG C-3' (FRAG. NO:1252) (SEQ. ID NO:1261)

5'-TGG CGG GCG TGG TGG CCT CTG TGG TGG-3' (FRAG. NO:1253) (SEQ. ID NO:1262)

50 5'-GGG CCC GCG GCT GCB GGG G-3' (FRAG. NO:1254) (SEQ. ID NO:1263)

5'-TTG CCT GTC TGC TTC GTC-3' (FRAG. NO:1255) (SEQ. ID NO:1264)

5'-CTT TGC GCT CCC GGG CCG CC-3' (FRAG. NO:1256) (SEQ. ID NO:1265)

5'-GGG GTG GGT AGG CCG TGT CTG GGG-3' (FRAG. NO:1257) (SEQ. ID NO:1266)

5'-GTT GGC CAT GTT GGT TGC C-3' (FRAG. NO:1258) (SEQ. ID NO:1267)

55 5'-GGG CCC GCG GCT GCA GGG G-3' (FRAG. NO:1259) (SEQ. ID NO:1268)

Human Fibronectin* Antisense Oligonucleotide Fragments

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CGC TGC CTT CTC CC CTC TCC TCG GCC GTT GCC TGT GC TGT CCG TCC TGT CGC CCT TCC GTG GTG C TGT
TGT CTC TTC TGC CCT C GGT GTG CTG GTG CTG GTG GTG CCT CTG CCC GTG CTC GCCCTG CCT GGG CTG
GCC TCT TCG GGT GTG GCT TTG GGG CTC TCT TGG TTG CCC TTT CTT CTC GTG GTG CCT CTC CTC CCT GGC
TTG GTC GT TGT CTG GGG TGG TGC TCC TCT CCC TTT CCC TGC TGG CCG TTT GT CCT GTT TTC TGT CTT
5 CCT CT TTC CTC CTG TTT CTC CGT TTG GCT TGC TGC TTG CGG GGC TGT CTC C CTT GCC CCT GTG GGC TTT
CCC TGG TCC GGT CTT CTC CTT GGG GGT C GCC CTT CTT GGT GGG CTGGCT CGT CTG TCT TTT TCC TTC C
TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1828) (SEQ.
ID NO: 1841)

- 5'-GGCCCCGGGC-3' (FRAG. NO:1829) (SEQ. ID NO: 1842)
- 10 5'-GCCGCGCGGGCG-3' (FRAG. NO:1830) (SEQ. ID NO:1843)
- 5'-GCCTGGGCTGGCC-3' (FRAG. NO:1831) (SEQ. ID NO: 1844)
- 5'-GGGGG TGGCCG-3' (FRAG. NO:1832) (SEQ. ID NO: 1845)
- 5'-GG GGG TGG CCG TTG TGG GCG G-3' (FRAG. NO:1833) (SEQ. ID NO: 1846)
- 5'-CGG TTT CCT TTG CGG TC-3' (FRAG. NO:1260)(SEQ. ID NO:1269)
- 15 5'-TTG GCC CGG GCT CCG GGT G-3' (FRAG. NO:1261)(SEQ. ID NO:1270)
- 5'-CCC GCC CGC CCG CCG GCC GCC GC-3' (FRAG. NO:1262)(SEQ. ID NO:1271)
- 5'-CCC GCC GGG CTG TCC CCG CCC CGC CCC-3' (FRAG. NO:1263)(SEQ. ID NO:1272)
- 5'-GGC CCG GGG CGC GGG GG-3' (FRAG. NO:1264)(SEQ. ID NO:1273)
- 5'-CGG CCC TCC CGC CCC TCT GG-3' (FRAG. NO:1265)(SEQ. ID NO:1274)
- 20 5'-GCC GGC GCG GGC GTC GG-3' (FRAG. NO:1266)(SEQ. ID NO:1275)
- 5'-CCG CTC GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C-3' (FRAG. NO:1267)(SEQ. ID NO:1276)
- 5'-GCC TGC CTC TTG CTC TTC-3' (FRAG. NO:1268)(SEQ. ID NO:1277)
- 5'-TGC GTC CGC TGC CTT CTC CC-3' (FRAG. NO:1269)(SEQ. ID NO:1278)
- 5'CTC TCC TCG GCC GTT GCC TGT GC-3' (FRAG. NO:1270)(SEQ. ID NO:1279)
- 25 5'-TGT CCG TCC TGT CGC CCT TCC GTG GTG C-3' (FRAG. NO:1271)(SEQ. ID NO:1280)
- 5'-TGT TGT CTC TTC TGC CCT C-3' (FRAG. NO:1272)(SEQ. ID NO:1281)
- 5'-GGT GTG CTG GTG CTG GTG GTG GTG-3' (FRAG. NO:1273)(SEQ. ID NO:1282)
- 5'-CCT CTG CCC GTG CTC GCC-3' (FRAG. NO:1274)(SEQ. ID NO:1283)
- 5'-CTG CCT GGG CTG GCC TCT TCG GGT-3' (FRAG. NO:1275)(SEQ. ID NO:1284)
- 30 5'-GTG GCT TTG GGG CTC TCT TGG TTG CCC TTT-3' (FRAG. NO:1276)(SEQ. ID NO:1285)
- 5'-CTT CTC GTG GTG CCT CTC CTC CCT GGC TTG GTC GT-3' (FRAG. NO:1277)(SEQ. ID NO:1286)
- 5'- TGT CTG GGG TGG TGC TCC TCT CCC-3' (FRAG. NO:1278)(SEQ. ID NO:1287)
- 5'-TTT CCC TGC TGG CCG TTT GT-3' (FRAG. NO:1279)(SEQ. ID NO:1288)
- 5'-CCT GTT TTC TGT CTT CCT CT-3' (FRAG. NO:1280)(SEQ. ID NO:1289)
- 35 5'-TTC CTC CTG TTT CTC CGT-3' (FRAG. NO:1281)(SEQ. ID NO:1290)
- 5'-TTG GCT TGC TGC TTG CGG GGC TGT CTC C-3' (FRAG. NO:1282)(SEQ. ID NO:1291)
- 5'-CTT GCC CCT GTG GGC TTT CCC-3' (FRAG. NO:1283)(SEQ. ID NO:1292)
- 5'-TGG TCC GGT CTT CTC CTT GGG GGT C-3' (FRAG. NO:1284)(SEQ. ID NO:1293)
- 5'-GCC CTT CTT GGT GGG CTG-3' (FRAG. NO:1285)(SEQ. ID NO:1294)
- 40 5'-GCT CGT CTG TCT TTT TCC TTC C-3' (FRAG. NO:1286)(SEQ. ID NO:1295)
- 5'-TGG GGG TGG CCG TTG TGG GCG GTG TGG TCC GCC T-3' (FRAG. NO:1287)(SEQ. ID NO:1296)
- 5'-TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1288)(SEQ. ID NO:1297)

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CAGCAAGACA CCTGTATCTA CAGAACAAGC CTCCAGGATT CATCAACACA AAGAGAAACT TTGTTTGGT
CCTGCTAAGG TGGAGGATTG AGGACATTAC TATTGCGTGG TAAGAAATTC ATCTTACTGC CTCAGAATTA
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55 ACTACCCGTT GCAGGAGACG GAGGACTTGT GTGCCCTTAT ATGGAGTTTT TTAATAATGA AAATAATGAG
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60 GTAATGTCAC CGGCCAGTTG AGTGACATTG CTTACTGGAA GTGGAATGGG TCAGTAATTG ATGAAGATGA
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 GACATTGTTG AGGTCATTAA TGAAAACGTA AAGAAAAGCA GAAGACTGAT TATCATTTTA GTCAGAGAAA
 CATCAGGCTT CAGCTGGCTG GGTGGTTCAT CTGAAGAGCA AATAGCCATG TATAATGCTC TTGTTACAGGA
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 TTCATTAAGC AGAAACATGG GGCTATCCGC TGGTCAGGGG ACTTTACACA GGGACCACAG TCTGCAAGA
 10 CAAGGTTCTG GAAGAATGTC AGGTACCACA TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAGTT
 ACTGTCACCA GCCACTAAGG AGAAACTGCA AAGAGAGGCT CACGTGCCTC TCGGGTAGCA TGGAGAAGTT
 GCCAAGAGTT CTTAGGTGC CTCCTGTCTT ATGGCGTTGC AGGCCAGGTT ATGCCTCATG CTGACTTGCA
 GAGTTCATGG AATGTAATA TATCATCCTT TATCCCTGAG GTCACCAGGA ATCAGG-3' (FRAG. NO:) (SEQ. ID
 NO:2519)

15 Human Interleukin-8* Fragments Antisense Oligonucleotide Fragments

5'-GBTGTTTGT BCCBBBGCBT CBBGBBTBGC TTTGCTBTCT BBGBTCBCB TTTBGBCBTB GBBBBBCGCT
 GTBGGTCBGBB BGBTGTGCTT BCCTTCBCB BGBGTGCBG BBTBCBGBBGG CTGCCBBGBGBG CCBCGGCCBGC
 TTGGBGTCBT GTTBCBCBC BGTGBGGTGC TCCGGTGGCT TTTTGCTTGT GTGCTCTGCT GTCTCTG TTC
 CTTCGGTGG TTTCTTCTG GCTCTGTCC TTTCTTGG CCCTTGGCCC-3' (FRAG. NO:1834) (SEQ. ID NO:1847)
 20 5'-G CTC CGG-3' (FRAG. NO:1835) (SEQ. ID NO:1848)
 5'-CBBGBBTBGC-3' (FRAG. NO:1836) (SEQ. ID NO:1849)
 5'-CBCBC BGTGBGGTGC-3' (FRAG. NO:1837) (SEQ. ID NO:1850)
 5'-BCCBBBGCBT CBBGBBTBGC-3' (FRAG. NO:1838) (SEQ. ID NO:1851)
 5'-GCCBBGBGBG CCBCGGCCBGC-3' (FRAG. NO:1839) (SEQ. ID NO:1852)
 25 5'-GTG CTC CGG TGG CTT TTT-3' (FRAG. NO:1289)(SEQ. ID NO:1298)
 5'-GCT TGT GTG CTC TGC TGT CTC TG-3' (FRAG. NO:1290)(SEQ. ID NO:1299)
 5'-TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' (FRAG. NO:1291)(SEQ. ID NO:1300)
 5'-TTC TCT TGG CCC TTG GCC C-3' (FRAG. NO:1292)(SEQ. ID NO:1301)
 5'-GBTGTTTGT BCCBBBGCBT CBBGBBTBGC TTTGCTBTCT BBGBTCBCB TTTBGBCBTB GBBBBBCGCT
 30 GTBGGTCBGBB BGBTGTGCTT BCCTTCBCB BGBGTGCBG BBTBCBGBBGG CTGCCBBGBGBG CCBCGGCCBGC
 TTGGBGTCBT GTTBCBCBC BGTGBGGTGC TCCGGTGGCT TTTTGCTTGT-3' (FRAG. NO:1840) (SEQ. ID NO:1853)

Human IL-8 Receptor Alpha Antisense Oligonucleotide Fragments

5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG
 GATCTGTAAT ATTTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGGB
 35 CBGGGGCTGT BBTCTTCBTC TGCBBGTGGC BTGCCBGTGB BBTBGBTC BTCBBBTCC CBCBTCTGTG
 GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG
 TGGCTCGGTG CTCTGCCCC GTTGTGTGCG GCGCTCGGT GGTGTGGCCC CTGTGGTGCT TCGTTTCCCC
 CTCTTCTCT TTGTTGCGGG GTTCTGTGG CGGGCTGCTT GTCTCGTTCC-3' (FRAG. NO:1841)(SEQ. ID NO:1854)
 5'-CBGGGGC-3' (FRAG. NO:1842) (SEQ. ID NO:1855)
 40 5'-GCBGGTGGC-3' (FRAG. NO:1843) (SEQ. ID NO:1856)
 5'-GCGGCGCTC-3' (FRAG. NO:1844) (SEQ. ID NO:1857)
 5'-TGGCTCGGTGCTTCTGCCCC (FRAG. NO:1293)(SEQ. ID NO:1302)
 5'-TGTTGTTGCGGCGCTC (FRAG. NO:1294)(SEQ. ID NO:1303)
 5'-GGTTGGTGTGGCCCTG (FRAG. NO:1295)(SEQ. ID NO:1304)
 45 5'-TGGTGCTTCGTTTCC (FRAG. NO:1296)(SEQ. ID NO:1305)
 5'-CCCTCTTCTCTTTGTTT (FRAG. NO:1297)(SEQ. ID NO:1306)
 5'-GGGGTCTTGTGTC (FRAG. NO:1298)(SEQ. ID NO:1307)
 5'-GGGCTGCTTGTCTCGTTCC (FRAG. NO:1299)(SEQ. ID NO:1308)
 5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG
 50 GATCTGTAAT ATTTGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CCGGCCAGG-3'
 (FRAG. NO:1845) (SEQ. ID NO:1858)
 5'-B CBGGGGCTGT BBTCTTCBTC TGCBBGTGGC BTGCCBGTGB BBTBGBTC BTCBBBTCC CBCBTCTGTG
 GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTC TBBCTGBBGC BCCGGCCBGG-3' (FRAG.
 NO:1846) (SEQ. ID NO:1859)

55 Interleukin-11 (IL-11) Nucleic Acid and Antisense Oligonucleotide Fragments

ACCTGGCCCC CCTCGAGTTT CCCAGACCC TCGGGCCGAG CTGGACAGCA CCGTGCTCCT GACCCGCTCT
 CTCCTGGCGG ACACGCGGCA GCTGGCTGCA CAGCTGAGGG ACAAATTCCC AGCTGACGGG GACCACAACC
 TGGATTCCCT GCCACCCTG GCCATGAGTG CGGGGGCACT GGGAGCTCTA CAGCTCCCAG GTGTGCTGAC
 AAGGCTGCGA GCGGACCTAC TGTCCTACCT GCGGCACGTG CAGTGGCTGC GCCGGGCGAGG TGGCTCTTCC
 5 CTGAAGACCC TGGAGCCCGA GCTGGGCACC CTGCAGGCCG GACTGGACCG GCTGCTGCGC CGGCTGCAGC
 TCCTGATGTC CCGCCTGGCC CTGCCCCAGC CACCCCCGGA CCCGCCGGCG CCCCCGCTGG CGCCCCCTC
 CTCAGCCTGG GGGGGCATCA GGGCCGCCCA CGCCATCCTG GGGGGGCTGC ACCTGACACT TGACTGGGCC
 GTGAGGGGAC TGCTGCTGCT GAAGACTCGG CTGTGACCCG GGGCCCAAAG CCACCACCGT CTTTCAAAG
 CCAGATCTTA TTTATTTATT TATTTAGTA CTGGGGCGA AACAGCCAGG TGATCCCCC GCCATTATCT
 10 CCCCCTAGTT AGAGACAGTC CTTCCGTGAG GCCTGGGGGA CATCTGTGCC TTATTTATAC TTATTTATTT
 CAGGAGCAGG GGTGGGAGGC AGGTGGACTC CTGGGTCCCC GAGGAGGAGG GGAAGGGAAG CCTGGGTTT
 TGGGTCTCCA AGAAGTCTGT CCACAGACTT CTGCCCTGGC TCTTCCCCAT CTAGGCCTGG GCAGGAACAT
 ATATTATTTA TTTAAGCAAT TACTTTTCAT GTTGGGGTGG GGACGGAGGG GAAAGGGAAG CCTGGGTTT
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 15 CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTTCCC CTCGGGGTCT CCCTGGGTCT
 CCCCAGTCC CTCCTGCTGT CTTCCCTCCG CTCTCTGATC TCTGACTCCC AGAACCTCTC CCTCTGTCTC
 CAGGGCTGCC CCTCTGATCC TCTTTGCTTC TCTGGTGTGT CTCTCTGGCT GCCTCCATCT CTGTGGATCT
 CCGTCTCCCT GTCTCTGTCT CAGTCTGTCC TTAAGTCTGT GTGTGTGTGT GTCTCTCTCT CTCTCTCTCC
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 20 TCTCTGCCTT TCCGTCTCTC TGCTTCCCA TCTCTCTCTG CTAGTCTGT CCAGCCGGAC CCCCACCCAC
 AGTCGGGCCC CAGCGCTTGA GCCTGAGTGT CTGCTCCGGC CCGTGGAGGT GGAGGGAGGG GACGCCAATG
 ACCTCACCAG CCCCTCTCCG ACCACCCCCC CCTTTCCTT TTCAACTTTT CCAACTTTTC CTTCCGTGCC
 CTCCTCCGAG CGCGGCGGGC TGAGCCCTGC AAGGCAGCCG CTCCGTCTGA ATGGAAAAGG CAGGCAGGGA
 GGGTGTGTC GATGTGTGCA GGCCGGCCCT CCCCTGCCGC CTGCCCCCG CCCGCCCGCC CCAGGCCCCC
 25 TATATAACCC CCCAGGCGTC CACTCTCCCT CACTGCCGCG GGCCCTGCTG CTCAGGGCAC ATGCCTCCCC
 TCCCCAGCCG CGGGCCAGC TGACCTCGG GGCTCCCCCG GCAGCGGACA GGAAGGGT AAAGGCCCCC
 GGCTCCCTGC CCCCTGCCCT GGGGAACCC TGGCCCTGTG GGGACATGAA CTGTAAGTTG GTTCATGGGG
 AGGGTGGAGG GGACAGGGAG GCAGGGAGGA GAGGGACCCA CGGCGGGGGT GGGAGCAGAC CCCGCTGAGT
 CGCACAGAGA GGGACCCGGA GACAGGCAGC CGGGGAGGAG AGCAGCTTCG GAGACAGGAG GCGGCGGAGG
 30 AGATGGGCAG AGAGAGACAC AGACAGGAGC GGATGGAGGC AGCCAATCAG AGGCGCCGCA GGAGGGACGG
 GCCAGACAGG GCCCAGAGG AGCGAGACGC GAGACCGAGC AGGGGCAGGG ACGCAGGGAC TGGTGCCGGG
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 40 TTCCCTGCT CCCAGCCAGC TCGGGCTCC GCGGCCGGG GAGGGGGCAG GTTCTGGCCT GTGCCTCCCC
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 45 CTCTCTCCC TCAGACCCAG GAGGAGTCCA GACCCAGTT CCTCTCCCT CAGACCCGGG AGTCCAGCCC
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 50 GAACGGAGAG GAGTCTGCG GCAGCCACTT GGAGGGGTT TGGGCTCTCA GGTGGCAGAG TGAGGGAGGG
 GAAGAGTTGG GGGCCTGGCG TGGGGGATGG AGGGAGCCCC GAGGCTGGGC AGGGGCCACC TCACAGCTTT
 TTCCCTGCC AGAGGGACAA ATTCCAGCT GACGGGGACC ACAACCTGGA TTCCCTGCCC ACCCTGGCCA

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 CTCCCAGGTG TGCTGACAAG GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC
 GGGCAGGTGG CTCTTCCCTG AAGACCCTGG AGCCCCGAGT GGGCACCTG CAGGCCCGAC TGGACCGCT
 10 GCTGCGCCGG CTGCAGCTCC TGGTATGTCC TGGCCCCAAG ACCTGACACC CCAGACCCCC ACCCTGGCC
 CCAAAATCCT GTGGCCTGAG TCCTTGAAGC CTGAGACCCC AGACCCGAGT GCAACAGCCC CGCTCTGAGA
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 ACAGTCCTGC TCTGAGACCC TGACCCTGCA GTCCCCAAGAT CCTGTGGCCC TGAGACCCTG AGGCCCTAGA
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 15 AGTCCCCAGA TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCAA AGCCTTGAGA ATTCAAATCC
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 25 CCAAAGCCCT GAGACCAGAA GACTTCAAAC CCTGGTTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA
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 40 TCACCTCTCT CCTCTCCCA CAGATGTCCC GCCTGGCCCT GCGCCAGCCA CCGCCGACC CGCCGCGGCC
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 45 ACTGGGGTCC CGGATTCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCCTGGCTC TTCCCCTCT
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5 TCTTTCTATA TATGGATTAA AACAAAAATC CTAAAGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC
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ACTGTGTTG CCGCCTGGTC CTGGTCGTGC TGAGCCTGTG GCCAGATACA GCTGTCGCCC CTGGGCCACC
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15 TGGATTCCCT GCCACCCTG GCCATGAGTG CGGGGGCACT GGGAGCTCTA CAGTCCCAG GTGTGCTGAC
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25 ATATTATTTA TTTAAGCAAT TACTTTTCAT GTTGGGGTGG GGACGGAGGG GAAAGGGAAG CTTGGGTTTT
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NO:) (SEQ. ID NO:2521)
5'-CAGCTGCGGC ATCCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCTTTCCC CTCGGGGTCT CCCTGGGTCT
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TCCTCCCCGA GACCCAGGAG TCCAGACCCC AGGCCTTCT CCTCAGACC TAGGAGTCCA GGCCCCAGC
CTCTCTCCC TCAGACCCAG GAGGAGTCCA GACCCAGTT CCTCCTCCCT CAGACCCGG AGTCCAGCCC
AGGCCCTCCT CTCTCAGACC CGGAGTCCAG CTTGAGCTCT CTGCCTTATC CTGCCCCAG GTGTTGCGC
60 CCTGGTCTG GTCGTGCTGA GCCTGTGGCC AGATACAGT GTCGCCCTG GGCCACCACC TGGCCCCCT

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CGAGTTTCCC CAGACCCTCG GGCCGAGCTG GACAGCACCG TGCTCCTGAC CCGCTCTCTC CTGGCGGACA
 CGCGGCAGCT GGCTGCACAG CTGGTAGGAG AGACTGGGCT GGGGCCAGCA CAGGAGTGAG AGGCAGAGAG
 GAACGGAGAG GAGTCTGCGG GCAGCCACTT GGAGGGGTTT TGGGCTCTCA GGTGGCAGAG TGAGGGAGGG
 5 GAAGAGTTGG GGGCCTGGCG TGGGGGATGG AGGGAGCCCC GAGGCTGGGC AGGGGCCACC TCACAGCTTT
 TTCCCTGCC AGAGGGACAA ATTCCAGCT GACGGGGACC ACAACCTGGA TTCCCTGCCC ACCCTGGCCA
 TGAGTGCAGG GGCAGTGGGA GCTCTACAGG TAAGGGCAAG GGAGTGGGCT GGGGACAAGG TGGGAGGCAG
 GCAGTGAAGG GGGCGGGGAG GATGAGGGG ACTGGTCGGG TGTTCTCTGA TGTCCCGGCT CTATCCCCAG
 CTCCAGGTG TGCTGACAAG GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC
 10 GGGCAGGTGG CTCTTCCCTG AAGACCCTGG AGCCCGAGCT GGGCACCCTG CAGGCCCGAC TGGACCGGCT
 GCTGCGCCGG CTGCAGCTCC TGGTATGTCC TGGCCCCAAG ACCTGACACC CCAGACCCCC ACCCTGGCC
 CCAAAATCCT GTGGCCTGAG TCCTTGAAGC CTGAGACCCC AGACCCGAGT GCAACAGCCC CGCTCTGAGA
 CCCTGACACC CTAACAGCCC GCTCTGAGAC CCTGACACCG TAACAGCCCC GCTCTGAGAC CCTGACCCTA
 ACAGTCTGCT TCTGAGACCC TGACCCTGCA GTCCCAAGAT CCTGTGGCCC TGAGACCCTG AGGCCCTAGA
 15 CCCCCAAATC CTGCCCAGAA ACTTCAAATT CTCACCCAAG ACCCTGAGAC TCCATCATCC ATGACCTCAA
 AGTCCCCAGA TCCCAGCCCC TAAGACCCAA GACCCCATCC TGAAGCCCCA AGCCTTGAGA ATTCAAATCC
 TCACCTCAAG ACTTGGAGAC CCTGGCCCCA TGACATTGAA AACCATGGAC CTGGCCAGGC GTGGTGGCTC
 ACGCCTGTAA TCCAGCACT TTGGGAGGCC GAGGCAAGTG GATCACCTGA GGTGGGAGT TCAAGACCAG
 CCAGACCAAC ATGGTGAAC CCTGTCTCTA CTAATAATAC AAAATTAGCC AGGCGTGGTG GTGCATGCCT
 20 GTAATCCCAG CTACTTGGGA GGCTGAGGCA GGAGAATCGC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG
 CCGAGATCGC ACCATTACAC TCCAGCCTGG GCAACAAGAG CAAAACCTCC TCTCTCTCAA AAAAAAAGAA
 AAAAAAAGAA AAGAAGGAAA AGAAAACCAT GGACCTCCAG ACCCTGAGAC CCCAGGCCCC AGCCCTGAGA
 TCCTGACATC TTAAAGATCC CAGGCCCTAA GATACAAGAC CTTGACCCAA AGCCAGCCTT GGGACCCTGG
 CTGTACAAAC CCAAGACCTC CAGGACCTAG ACCCCGAGCC CTGAGGCCCT ATGTCTCACT CCCAACATCG
 25 AAAACCTGAA CACCTCAGAT CCTGAGCCTG CGCCTGTACG ACTCCAAGAC CCTCACTTCC AAAGCCAGGC
 CCAAAGCCCT GAGACCAGAA GACTTCAAAC CCTGGTCTT GGGCCTAACT CCAAAGACCC TGGATCTCAA
 ATTCCAACCT CTAGCTCTGA GACTCCAGCC CTCACCATG AGTTCCTGAA CTTGAACCCA GAGACCCCAT
 CTCTAAGACT TCAGCCTTGA GATCCAGGGC CTGACCCTAG ACTCGAGCCC ACAGACCTCA GATACTGTCT
 GTAAAAACCC AGCTCTGGTG GGGAGCAGTG GCTCACTCCT GTAATCCCAA GGCAGGGGAG GCCAAGGCAG
 30 AAGGACCTCT TGAGGCCATG AGTTTGAGAC AGCCTGGGCA GCATAGCAAG ACTCTGTTTC TTAATTATTA
 TTATTATTAT TATTTTTTGG AGACAGAGTC TCGCGCTCTG TTGCCCAGGC TAGAGTGCAA TGGTGCCATT
 TCGGCTTGCT GGAACCTCCG CCTCCTGGGC TCAAGCGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA
 CTTCAAGTGG CACTTGCCAC ACCCGGATAA TTTTPTTGTA TTTTAGTAGA CACAGGGTTT CACCGTGTG
 CCCAGGCTGG TCACAAACTC CTGAGCTCAG GCCATCCGCC CGCCTCGGCC TCCCAAAGCG CTGGGATAAC
 35 AGGCGTGACG CCGCGCCTGG CTTCTTAATT GTTCTAAGC CAGCGACAAC AACAAAAACC CAGCTCTGAG
 ATTCCAGCCC CGGCGACTCT AACAGTCCCA GGCCCGATCC CTCACCTAGA ACCGAGTAGC CAGCCCTGAC
 TCCACAGACT TCACCCCCAA CCCCCACACT CAGCTCTGGA AGCCCGTCTT GACTCCAGCC TCCATTTTCG
 GAACCCCAACA GCCTGAAGAG CTCCCGGCCT AAACACTTCA CCCCACGCGC CACAGTCCCC CTGTGAATAT
 GCAGCCCCGA TTCAGCTGCA GCTCCACAGC ACCCTGCCCC TGCACCCCCG CTGCACCCCC TACCTGTGAC
 40 TCACCTCTCT CCTCTCCCCA CAGATGTCCC GCCTGGCCCT GCCCAGCCA CCCCAGGACC CGCCGGCGCC
 CCCGCTGGCG CCCCCCTCCT CAGCCTGGGG GGGCATCAGG GCCGCCCACG CCATCCTGGG GGGGCTGCAC
 CTGACACTTG ACTGGGCCGT GAGGGGACTG CTGCTGCTGA AGACTCGGCT GTGACCCGGG GCCCAAAGCC
 ACCACCTGCC TTCCAAAGCC AGATCTTATT TATTTATTTA TTTCAGTACT GGGGGCGAAA CAGCCAGGTG
 ATCCCCCGCG CATTATCTCC CCCTAGTTAG AGACAGTCTT TCCGTGAGGC CTGGGGGGCA TCTGTGCCTT
 45 ATTTATACTT ATTTATTTCA GGAGCAGGGG TGGGAGGCAG GTGGACTCCT GGGTCCCCGA GGAGAGGGG
 ACTGGGGTCC CGGATTCTTG GGTCTCCAAG AAGTCTGTCC ACAGACTTCT GCCCTGGCTC TTCCCCATCT
 AGGCCTGGGC AGGAACATAT ATTATTTATT TAAGCAATTA CTTTTCATGT TGGGGTGGGG ACGGAGGGGA
 AAGGGAAGCC TGGGTPTTTG TACAAAAATG TGAGAAACCT TTGTGAGACA GAGAACAGGG AATTAAATGT
 GTCATACATA TCCACTTGAG GGCGATTTGT CTGAGAGCTG GGGCTGGATG CTTGGGTAAC TGGGGCAGGG
 50 CAGGTGGAGG GGAGACCTCC ATTCAGGTGG AGGTCCCGAG TGGGCGGGGC AGCGACTGGG AGATGGGTG
 GTCACCCAGA CAGCTCTGTG GAGGCAGGTG CTGAGCCTTG CCTGGGGCCC CGCACTGCAT AGGGCCGTTT
 GTTTGTPTTT TGAGATGGAG TCTCGCTCTG TTGCTAGGCG TGGAGTGCAG TGAGGCAATC TAAGGTCACT
 GCAACCTCCA CCTCCGGGT TCAAGCAATT CTCTGCTCTC TTTTGTATT TTAGTAGAG ACAGGGTTTC TCACAGGTG
 GCACCAACAT GCCCAGCTAA TTATTTATTT CTTTGTATT TTAGTAGAG ACAGGGTTTC ACCATGTTGG
 55 CCAGGCTGGT TTCGAACTCC TGACCTCAGG TGATCCTCCT GCCTCGGCCT CCCAAAGTGC TGGGATTACA
 GGTGTGAGCC ACCACACCTG ACCCATAGGT CTTCAATAAA TATTTAATGG AAGGTTCCAC AAGTCAACCCT
 GTGATCAACA GTACCCGTAT ATATCCAACA GTGAGGGTTA AGCAACATGG TGCATCTGTG GATAGAACGC
 GCAAACCTGGA AACAATCTAG CCCGGAGCAG GGACTGTCTC TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA
 CACCCAGCCG CCGGAGCAG ACATTGGCCA GGCATGGTGG CTCACGCTCG TAATCCTGGC ACTTTGGGAG GACGAAGCGA
 60 AGATATCCTG AGATTGGCCA AGTTTGAGAC CGGCCTCGGA GACATGGCAA AACCTGTCT CAAAAAGAA
 GTGGATCACT GAAGTCCAAG CCTGACATGA AACAGCAGGC TACAAAACCA CTGCATGCTG TGTGTGTTT
 AGAATGATGT CCTGACATGA AACAGCAGGC TACAAAACCA ATACGCCAAA ATGTTGACAA TGACTGTCTC
 TCTTTCTATA TATGGATTAA AACAAAAATC CTAAGGGGAA ATACGCCAAA ATGTTGACAA TGACTGTCTC

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CAGGTCAAAG GAGAGAGGTG GGATTGTGGG TGACTTTTAA TGTGTATGAT TGTCTGTATT TTACAGAATT
TCTGCCATGA CTGTGTATTT TGCATGACAC ATTTTAAAAA TAATAAACAC TATTTTAGA ATAACAGAAT
ATCAGCCTCC TCCTCTCCAA AAATAAGCCC TCAGGAGGGG ACAAAGTTGA CCGCTGATTG AGCCTGTCAG
GGCTGTGCAC-3' (FRAG. NO:_) (SEQ. ID NO:2522)

5 **Human GM-CSF Nucleic Acid and Antisense Oligonucleotide Fragments**

- 5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCTGCBC TGTCCBGBGT
GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG
GTCTGGGTGG GGCTGGGCTG CBGGCTCCGG GCGGTCCBGCCBTGGGTCTG GGGGCTGGG CTGCBGGCTC
CGGGCGGGCG GGTGCGGGCT GCGTGTGGG GGCTGCCCCG CAGGCCCTGC GGTCCBGGCB TGGGTCTGGG
10 GGCTGGGCTG CBGGCTCCGG GCGGGCGGGT GCGGGCTGCG TGCTGGGGGC TGCCCCGAG GCCTGC-3' (FRAG.
NO:1847) (SEQ. ID NO:1860)
5'-GBGCBGG BBG-3' (FRAG. NO:1848) (SEQ. ID NO:1861)
5'-GCCBCBGCBCBGC-3' (FRAG. NO:1849) (SEQ. ID NO:1862)
5'-GGG TGC GGG C-3' (FRAG. NO:1850) (SEQ. ID NO:1863)
15 5'-GGT CCB GCC BTG GGT CTG GG-3' (FRAG. NO:1300)(SEQ. ID NO:1309)
5'-GGC TGG GCT GCB GGC TCC GG-3' (FRAG. NO:1301)(SEQ. ID NO:1310)
5'-GCG GGC GGG TGC GGG CTG CGT GCT GGG-3' (FRAG. NO:1302)(SEQ. ID NO:1311)
5'-GGC TGC CCC GCA GGC CCT GC-3' (FRAG. NO:1303)(SEQ. ID NO:1312)
5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBGGGCCC BGGGGGGTGG CTTCTGCBC TGTCCBGBGT
20 GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG
GTCTGGGTGG GGCTGGGCTG CBGGCTCCGG GC-3' (FRAG. NO:1851) (SEQ. ID NO:1864)

Human Tumor Necrosis Factor α Antisense Oligonucleotide Fragments

- 5'-GCBCCGCTG GBGCCCTGGG GCCCCCTGT CTCTTGGGG BGCCTCCT CGGCCBGTG CBCGTCCCGG
BTCBTGCTTT CBGTGCTCBT GGTGTCTTT CCBGGGBGB GBGGGGCTGG TCCTGTCTG TCCTGTCTGG
25 TGCTCBTGGT GTCCTTTCCG CCCTGGGGCC CCCGTGTCTT CTGGGGCTT CTCCCTCTG GGGGCCGTCT
CTCTCCCTCT CTTCGCTCTC TCTTTTCTC TCTCTCTCT CCCCTTCC GCTCTTCTG TCTCGGTGTC
TGGTTTCTC TCTCCGCTGG CTGCTGTCT GGCTGCGCT CTGCGCTGT GCTGTCTCTC CTCCGTTCC
TGCTCTCTCT GTCTGTGCGC CCCTCTGGGG TCTCCCTCTG GGTGGTGGTC TTGTGTCTG GGCTGGGCTC
CGTGTCTCCB GTGCTCBTGG TGTCCGCTGB GGBGCGTCT GCTGGCGCTG GTCCTCTGCTGTC CTGCTGGTG
30 CTCBTGGTGT CCTTCCGCC CTGGGGCCCC CCTGTCTTCT TGGGGCCTCT TCCCTCTGGG GGCGTCTC
TCTCCCTCTC TTGCGTCTCT CTCTTCTCT CTCTCTCTC CCCTTCCCG CTCTTCTGT CTCGGTGTCT
GGTTTCTCT CTCCGCTGGC TGCTGTCTG GCCTGCGCTC TTGGCCTGTG CTGTTCTCTC TCCGGTTCTC
GTCCTCTCTG TCTGTGCGCC CCTCTGGGT CTCCCTCTG CGTGGTGGTC TTGTGTCTG GGCTGGGCTC
CGTGTCTCCB GTGCTCBTGG TGTCCGCTGB GGBGCGTCT GCTGGC-3' (FRAG.NO:1852)(SEQ.ID NO:1865)
35 5'-GGGGCCCCC-3' (FRAG. NO:1853) (SEQ. ID NO:1866)
5'- GGG GGC CG TCT-3' (FRAG. NO:1854) (SEQ. ID NO:1867)
5'-CCBGGGBGB GBGGGGCTGG-3' (FRAG. NO:1855) (SEQ. ID NO:1868)
5'-GCBCCGCTG GBGCCCTGGG GCCCCCTGT CTCTTGGGG BGCCTCCT CGGCCBGTG CBCGTCCCGG
BTCBTGCTTT CBGTGCTCBT GGTGTCTTT CCBGGGBGB GBGGG-3' (FRAG. NO:1304) (SEQ. ID NO:1313)
40 5'-GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC CTG GGG CCC CCC TGT CTT CTT
GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT C TCT TTC TCT CTC TCT CTT CCC
C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC TGC CTG TCT GGC CTG CGC TCT T
GGC CTG TGC TGT TCC TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC CCC TCT GGG GTC TCC CTC TGG C
GTG GTG GTC TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB TGG TGT CC-3' (FRAG. NO:1305)
45 (SEQ. ID NO:1314)
5'-GCT GBG GGB GCG TCT GCT GGC GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC
CTG GGG CCC CCC TGT CTT CTT GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT TGC GTC TCT
C TCT TTC TCT CTC TCT CTT CCC C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC
TGC CTG TCT GGC CTG CGC TCT T GGC CTG TGC TGT TCC TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC
50 CCC TCT GGG GTC TCC CTC TGG C GTG GTG GTC TTG TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB
TGG TGT CC GCT GBG GGB GCG TCT GCT GGC-3' (FRAG.NO:1306)(SEQ.ID NO:1315)
5'-GCT GGT CCT CTG CTG TCC TTG CTG-3' (FRAG. NO:1655) (SEQ. ID NO:1664)
5'-GTG CTC BTG GTG TCC TTT CC-3' (FRAG. NO:1656)(SEQ. ID NO:1665)
5'-GCC CTG GGG CCC CCC TGT CTT CTT GGG G-3' (FRAG. NO:1657)(SEQ. ID NO:1666)
55 5'-CCT CTT CCC TCT GGG GGC CG-3' (FRAG. NO:1658)(SEQ. ID NO:1667)
5'-TCT CTC TCC CTC TCT TGC GTC TCT C-3' (FRAG. NO:1659)(SEQ. ID NO:1668)
5'-TCT TTC TCT CTC TCT CTT CCC C-3' (FRAG. NO:1660)(SEQ. ID NO:1669)
5'-TTT CCC GCT CTT TCT GTC TC-3' (FRAG. NO:1661)(SEQ. ID NO:1670)
5'-GGT GTC TGG TTT TCT CTC TCC-3' (FRAG. NO:1662)(SEQ. ID NO:1671)

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- 5'-GCT GGC TGC CTG TCT GGC CTG CGC TCT T-3' (FRAG. NO:1663)(SEQ. ID NO:1672)
 5'-GGC CTG TGC TGT TCC TCC-3' (FRAG. NO:1664)(SEQ. ID NO:1673)
 5'-TCC GGT TCC TGT CCT CTC TGT CTG TC-3' (FRAG. NO:1665)(SEQ. ID NO:1674)
 5'-GCC CCC TCT GGG GTC TCC CTC TGG C-3' (FRAG. NO:1666)(SEQ. ID NO:1675)
 5'-GTG GTG GTC TTG TTG CTT-3' (FRAG. NO:1667)(SEQ. ID NO:1676)
 5'-GGG CTG GGC TCC GTG TCT C-3' (FRAG. NO:1668)(SEQ. ID NO:1677)
 5'-CBG TGC TCB TGG TGT CC-3' (FRAG. NO:1669)(SEQ. ID NO:1678)
 5'-GCT GBG GGB GCG TCT GCT GGC-3' (FRAG. NO:1670)(SEQ. ID NO:1679)

Human Leukotriene C4 Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

- 10 5'-CTCGGTBGC GCGCTCBBB TCGGGTGGG CGGTGGTGBG CGGCGGCBBCB CGCGBBGGC CCTGCGCGCC
 GBGBTCBCCTG CBGGGBBBG TBGGCTTGCB GCBGBCTCC CBGGGGGTG BCBGCBGCCB GTBGBGCTBC
 CTCGTCTTC BTGGTBCCGT CGGTGTGGTG GCBGGGCTG TGTGTBBGG CGBGCTGGC CCCGTCTGCT
 GCTCCTCGTG CCGCCTCGTC CTCA TGG TA CCGTCGGTGT GGTGGCCTCG GGTGGGCCG TGGTGGGGCG
 CGCGGCTCG CGTGGCTCCG GCTCTTCTT CCCGGCTCCGT CGGCCCGGG GCCTTGGTCT CCCTCGTCTC
 15 TCBTGGTBCC G-3' (FRAG. NO:1856) (SEQ ID NO: 1869)
 5'-GCB GCBGGBC-3' (FRAG. NO:1857) (SEQ ID NO: 1870)
 5'-CCCGGCTCCG-3' (FRAG. NO:1858) (SEQ ID NO: 1871)
 5'-CGGCCCGGG GCC-3' (FRAG. NO:1859) (SEQ ID NO:1872)
 5'-CB CGCG-3' (FRAG. NO:1860) (SEQ ID NO: 1873)
 20 5'-GCC CCG TCT GCT GCT CCT CGT GCC G-3' (FRAG. NO:1307)(SEQ. ID NO:1316)
 5'-CCT CGT CCT TCA TGG TAC CGT CGG TGT GGT GGC-3' (FRAG. NO:1308)(SEQ. ID NO:1317)
 5'-CTC GGG TGG GCC GGT GGT G-3' (FRAG. NO:1309)(SEQ. ID NO:1318)
 5'-GGG GCG GCG CGC TCG CGT-3' (FRAG. NO:1310)(SEQ. ID NO:1319)
 5'-GGC TCC GGC TCT TCT TTC CCG GCT CCG TCG GCC CGG GGT CCT TGG TCT C-3'(FRAG.NO:1311)(SEQ.ID NO:1320)
 25 5'-CCT CGT CCT TCB TGG TBC CG-3' (FRAG. NO:1312)(SEQ. ID NO:1321)
 5'-CTCGGTBGC GCGCTCBBB TCGGGTGGG CGGTGGTGBG CGGCGGCBBCB CGCGBBGGC CCTGCGCGCC
 GBGBTCBCCTG CBGGGBBBG TBGGCTTGCB GCBGBCTCC CBGGGGGTG BCBGCBGCCB GTBGBGCTBC
 CTCGTCTTC BTGGTBCCGT CGGTGTGGTG GCBGGGCTG TGTGTBBGG CGBGCTGG-3' (FRAG.NO:1861)
 (SEQ ID NO:1874)

Human Endothelin-1 Nucleic Acids and Antisense Oligonucleotide Fragments

- 30 5'-BCCGGCGBG CCGCCBGGT GGBCTGGBG TGGTTCCTC CCCGCCGTC TCBCCBCCG CGCTGBGCTC
 BGCCTBBG BCTGCTGTT CTGGGCTCC TTGGCBGCC BCBBCBGC BCBGBBBBT CBTGBGCB
 TBBTCCBTTC TGBBBBBBBB GGBTCBBBB CCTCCCGTTC CCCGTTGCC TGGCGCGCGC TGCGGGTTCC
 TCGTGGGTT CTCCCCCGG TTCTCCGGTC TGTTGCTTT GTGGGCTTCT TGTCCTTTTG GCTGTCTTT
 35 TCCTGCTTG CGTCTTTTCC TTTCTTTGTG CTCGGTTGT GGTCCGCTGG TCCTTTGCC TGTGTGTTT
 TGCTGCCCGT TCGCTGGCG CGCGCTGCG GTTCTCTGT GGTTCCTCC CGCGTTCTC CGGTCTGTTG
 CCTTTGTTG CTTCTGTCT TTTGGCTGT TCTTTCTGT CTGGCGTCT TTTCTTTCT TTGTGCTCGG
 TTGTGGTCC GCTGTCCTT TGCCCTGTG GTTCTGCTG-3' (FRAG. NO:1862) (SEQ. ID NO:1875)
 5'-CCGGCGBG CCGCCBGGT GGB-3' (FRAG. NO:1863) (SEQ. ID NO:1876)
 40 5'-CCGCCBGGG-3' (FRAG. NO:1864) (SEQ. ID NO:1877)
 5'-GGCGCGCGC-3' (FRAG. NO:1865) (SEQ. ID NO:1878)
 5'-GTGGTCCGC-3' (FRAG. NO:1866) (SEQ. ID NO:1879)
 5'-CCCGTTCGCTGGCGC-3' (FRAG. NO:1313)(SEQ. ID NO:1322)
 5'-GCGCTGCGGGTTCCTC-3' (FRAG. NO:1314)(SEQ. ID NO:1323)
 45 5'-GTGGGTTTCTCCCCCGGTTCTC-3' (FRAG. NO:1315)(SEQ. ID NO:1324)
 5'-CGGTCTGTTGCTTTGTGGG-3' (FRAG. NO:1316)(SEQ. ID NO:1325)
 5'-CTTCTGTCTTTTGGCT-3' (FRAG. NO:1317)(SEQ. ID NO:1326)
 5'-GTTCTTTCTGCTTGGC-3' (FRAG. NO:1318)(SEQ. ID NO:1327)
 5'-GTCTTTCTTTCTT-3' (FRAG. NO:1319)(SEQ. ID NO:1328)
 50 5'-TGTGCTCGGTTGTGGTC-3' (FRAG. NO:1320)(SEQ. ID NO:1329)
 5'-CGTGGTCTTTGCC-3' (FRAG. NO:1321)(SEQ. ID NO:1330)
 5'-CTGTGTGTTTCTGCTG-3' (FRAG. NO:1322)(SEQ. ID NO:1331)
 5'-CCCGTTCGCTGGCGC-3' (FRAG. NO:1323)(SEQ. ID NO:1332)
 5'-GCGCTGCGGGTTCCTC-3' (FRAG. NO:1324)(SEQ. ID NO:1333)
 55 5'-GTGGGTTTCTCCCCCGGTTCTC-3' (FRAG. NO:1325)(SEQ. ID NO:1334)
 5'-CGGTCTGTTGCTTTGTGGG-3' (FRAG. NO:1326)(SEQ. ID NO:1335)
 5'-CTTCTGTCTTTTGGCT-3' (FRAG. NO:1327)(SEQ. ID NO:1336)
 5'-GTTCTTTCTGCTTGGC-3' (FRAG. NO:1328)(SEQ. ID NO:1337)
 5'-GTCTTTCTTTCTT-3' (FRAG. NO:1329)(SEQ. ID NO:1338)
 60 5'-TGTGCTCGGTTGTGGTC-3' (FRAG. NO:1330)(SEQ. ID NO:1339)

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5'-CGCTGGTCCTTTGCC-3' (FRAG. NO:1331)(SEQ. ID NO:1340)

5'-CTGTGTGTTTCTGCTG-3' (FRAG. NO:1332)(SEQ. ID NO:1341)

Endothelin Receptor ET-B Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-GCCCTGTCGG GCGGGAAGCC TCTCTCCTCT CCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA
5 ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC
GCCGCGCC CTGTGCGGCG GBBGCTCT CTCCTCTCCC CBGBTCCGCG BCBGGCCGCB GGCBBGBBCC
BGCGBBCCB GGGCGCGTCC GCBCGBCTT GBBGGCGGCT GCBTGCTGCT BCCTGCTCGGGCG GBBGCTCCG
GTGGCCGCCG CGCTCCGGT GGCCGCCGCG CCTCTCTCT CTCCCCGTGG CCTGTGCGG CGGGTCTGCT
CGTCTGTCT CTTTTCTTT TGCTGTCTTG TCTCCCGTC TGTCTTT-3' (FRAG. NO: 1867) (SEQ. ID NO: 1880)
- 10 5'-CGGGCG GBBGCC-3' (FRAG. NO: 1868) (SEQ. ID NO: 1881)
5'-CGGGCGG-3' (FRAG. NO: 1869) (SEQ. ID NO: 1882)
5'-CCGCBGBGC-3' (FRAG. NO: 1870) (SEQ. ID NO: 1883)
5'-GCTCCGGTGGCCCGC-3' (FRAG. NO:1333)(SEQ. ID NO:1342)
5'-GCCTCTCTCTCTCCC-3' (FRAG. NO:1334)(SEQ. ID NO:1343)
- 15 5'-GTGGCCCTGTGCGGCGGG-3' (FRAG. NO:1335)(SEQ. ID NO:1344)
5'-TCCTGCCGTCTGTCTCTTT-3' (FRAG. NO:1336)(SEQ. ID NO:1345)
5'-TCTTTGCTGTCTTG-3' (FRAG. NO:1337)(SEQ. ID NO:1346)
5'-CTTCCGTCTGTCTTT-3' (FRAG. NO:1338)(SEQ. ID NO:1347)
5'-GCCCTGTCGG GCGGGAAGCC TCTCTCCTCT CCCAGATC CGCGACAGGC CGCAGGCAAG AACCAGCGCA
20 ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC
GCCG-3' (FRAG. NO: 1871) (SEQ. ID NO: 1884)
5'-GCCCTGTCGG GCGGGBGCC TCTCTCCTCT CCCBGBTCC GCGBCGGCC GCBGGCBGB BCCBGCGB
BCCBGGGCGC GTCCGCBGB BCTTGGGGC GGCTGCBTGC TGCTBCCTGC TCCBGBGCG TCCGGTGGCC GCCG-
3' (FRAG. NO: 1872) (SEQ. ID NO: 1885)

Endothelin ETA Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-GTCTGTCCT CCCGTCTCT CCACTGCTT CTCCCGGGG CTTCGCCGGC TTCGGGTGGC CGGTGTCCCG
GGCTCCGGCG CGGCGGCGGC TTCGGTGGC GGTGGGTGGC GCGGGCTGCC GGGTCCGCGC GGCGCTGGG
CCCTGTGCT GCTTTTGTG TGTTCCGTT TGGTGTCTC GGTCTGTGT GTGGTGTGT TGTCTCTCT
TGGGTGTGG CTTGCGGTT TTGGCTGTG GCCCTTGGG GCCTTGGCT CTGGCTCGTC TGTCTCCCC
30 GTCTCTCCC ACTGCTTCT CCCGGGGGCT TCCCGGCTT CGGGTGGCCG GTGTCCCGG CTCCGGCGCG
GCGGCGGCTT CGGTGCGGG TGGTGGCGC GGGTGGCGG GTCCGCGCG CGCTGGGCT CTTGTGCTGC
TTTTGCTTG TTCCGTTCTG GCTGCTCCG TCTGTGTTG GGTGTGTTT TTTCTCTTG GGTGTGGGC
TTGCGGTTT GGCTGTGGC CCTTGGGGC CTGGCTTCT GGCTCCAT CCACATGATT GCTTAGATT
GTGCTGATC TCTCAGGATT ATCACTGATT ACACATCAA CCAGTGCCAG CCAAAGGAT GCCCTGAGGC
35 AAAGGGTTT CATCTGAGG CAAATTGAG GACBTCCBC BTGBTTGCTT BGTGTTGTG TGTBTCTCT
BGBTTBTB CTGBTTBCB BTCCBBCCG TGCCBGCCB BBGGTGCC TGBGGCBGB GGTTCBCTC
TTGBGGCBB TTBGGGB-3' (FRAG. NO:1873) (SEQ. ID NO: 1886)
5'-GBGGCBGBGG-3' (FRAG. NO:1874) (SEQ. ID NO: 1887)
5'-GCCBGCCB BBGB-3' (FRAG. NO:1875) (SEQ. ID NO: 1888)
- 40 5'-CGCCTGGGCC C-3' (FRAG. NO:1876) (SEQ. ID NO: 1889)
5'-GTCTGTCCTCCCGTCTCTCCC-3' (FRAG. NO:1339)(SEQ. ID NO:1348)
5'-ACTGCTTCTCCGGGG-3' (FRAG. NO:1340)(SEQ. ID NO:1349)
5'-GCTTCCCGGCTTC-3' (FRAG. NO:1341)(SEQ. ID NO:1350)
5'-GGGTGGCCGGTGTCCCGGGCTCCGGCGCGCGGC-3' (FRAG. NO:1342)(SEQ. ID NO:1351)
- 45 5'-GGCTTCGGCTGC-3' (FRAG. NO:1343)(SEQ. ID NO:1352)
5'-GGGTGGGTGGCGCG-3' (FRAG. NO:1344)(SEQ. ID NO:1353)
5'-GCTGCCGGGTCCGCGCGGCGCTGGGCC-3' (FRAG. NO:1345)(SEQ. ID NO:1354)
5'-CTTCTCTCTCTTT-3' (FRAG. NO:1346)(SEQ. ID NO:1355)

Endothelin Receptor A Nucleic Acid and Antisense Oligonucleotide Fragments

	5'-GCCACCATGG	AAACCCTTTG	CCTCAGGGCA	TCCTTTTGGC	TGGCACTGGT	TGGATGTGTA	ATCAGTGATA
	ATCCTGAGAG	ATACAGCACA	AATCTAAGCA	ATCATGTGGA	TGATTTACC	ACTTTTCGTG	GCACAGAGCT
	CAGCTTCCTG	GTTACCACTC	ATCAACCCAC	TAATTTGGTC	CTACCCAGCA	ATGGCTCAAT	GCACAACTAT
5	TGCCCACAGC	AGACTAAAAT	TACTTCAGCT	TTCAAATACA	TTAACTGT	GATATCTTGT	ACTATTTTCA
	TCGTGGGAAT	GGTGGGGAAT	GCAACTCTGC	TCAGGATCAT	TTACCAGAAC	AAATGTATGA	GGAATGGCCC
	CAACGCGCTG	ATAGCCAGTC	TTGCCCTTGG	AGACCTTATC	TATGTGGTCA	TTGATCTCCC	TATCAATGTA
	TGGCTGGGCG	CTGGCCTTTT	GATCACAATG	ACTTTGGCGT	ATTTCTTTGC	AAGCTGTTC	CCTTTTTCGA
	GAAGTCCTCG	GTGGGGATCA	CCGTCCTCAA	CCTCTGCGCT	CTTAGTGTTG	ACAGGTACAG	AGCAGTTGCC
10	TCCTGGAGTC	GTGTTCAGGG	AATTGGGATT	CCTTTGGTAA	CTGCCATTGA	AATTGCCTCC	ATCTGGATCC
	TGTCCTTTAT	CCTGGCCATT	CCTGAAGCGA	TGGCTTCGT	CATGGTACCC	TTTGAATATA	GGGGTGGACA
	GCATAAAACC	TGTATGCTCA	ATGCCACATC	AAAATTCATG	GAGTTCTACC	AAGATGTAAA	GGACTGGTGG
	CTCTTCGGGT	TCTATTTCTG	TATGCCCTTG	GTGTGCACTG	CGATCTTCTA	CACCCTCATG	ACTGGTGAGA
	TGTTGAACAG	AAGGAATGGC	AGCTTGAGAA	TTGCCCTCAG	TGAACATCTT	AAGCAGCGTC	GAGAAGTGGC
15	AAAAACAGTT	TTCTGCTTGG	TTGTAATTTT	TGCTCTTTGC	TGGTTCCCTC	TTCATTTAAG	CCGTATATTG
	AAGAAAACCTG	TGTATAACGA	GATGGACAAG	AACCGATGTG	AATTACTTAG	TTTCTTACTG	CTCATGGATT
	ACATCGGTAT	TAACCTGGCA	ACCATGAATT	CATGTATAAA	CCCCATAGCT	CTGTATTTTG	TGAGCAAGAA
	ATTTAAAAAT	TGTTTCCAGT	CATGCCTCTG	CTGCTGCTGT	TACCAGTCCA	AAAGTCTGAT	GACCTCGGTC
	CCCATGAACG	GAACAAGCAT	CCAGTGGAAG	AACCACGATC	AAAACAACCA	CAACACAGAC	CGGAGCAGCC
20	ATAAGGACAG	CATGAACTGA	CCACCCTTAG	AAGCACTCCT	GAATTCGGGA	AAAAGTGAAG	GTGTAAAAGC
	AGCACAAGTG	CAATAAGAGA	TATTTCTCTA	AATTTGCCTC	AAGATGGAAA	CCCTTGCCT	CAGGGCATCC
	TTTTGGCTGG	CACTGGTTGG	ATGTGTAATC	AGTGATAATC	CTGAGAGATA	CAGCACAAAT	CTAAGCAATC
	ATGTGGATGA	TTTACCACCT	TTTCGTGGCA	CAGAGCTCAG	CTTCCTGGTT	ACCACTCATC	AACCCACTAA
	TTTGGTCCTA	CCCAGCAATG	GCTCAATGCA	CAACTATTGC	CCACAGCAGA	CTAAAATTAC	TTCAGCTTTC
25	AAATACATTA	ACACTGTGAT	ATCTTGTAAT	ATTTTCATCG	TGGGAATGGT	GGGGAATGCA	ACTCTGCTCA
	GGATCATTTA	CCAGAACAAA	TGTATGAGGA	ATGGCCCCAA	CGCGCTGATA	GCCAGTCTTG	CCCTTGGAGA
	CCTTATCTAT	GTGGTCATTG	ATCTCCCTAT	CAATGTATTT	AAGCTGCTGG	CTGGGCGCTG	GCCTTTTGAT
	CACAATGACT	TTGGCGTATT	TCTTTGCAAG	CTGTTCCCTT	TTTTCAGAA	GTCCTCGGTG	GGGATCACCG
	TCCTCAACCT	CTGCGCTCTT	AGTGTGACA	GGTACAGAGC	AGTTGCCTCC	TGGAGTCGTG	TTCAGGGAAT
30	TGGGATTCCCT	TTGGTAACTG	CCATTGAAAT	TGTCTCCATC	TGGATCCTGT	CCTTTATCCT	GGCCATTCCCT
	GAAGCGATTG	GCTTCGTCAT	GGTACCCTTT	GAATATAGGG	GTGAACAGCA	TAAAACCTGT	ATGCTCAATG
	CCACATCAAA	ATTATGAGAG	TTCTACCAAG	ATGTAAAAGGA	CTGGTGGCTC	TTCGGGTTCT	ATTTCTGTAT
	GCCCTTGGTG	TGCACTGCGA	TCTTCTACAC	CCTCATGACT	TGTGAGATGT	TGAACAGAAG	GAATGGCAGC
	TTGAGAATTG	CCCTCAGTGA	ACATCTTAAG	CAGCGTCGAG	AAGTGGCAAA	AACAGTTTTT	TGCTTGGTTG
35	TAATTTTTGC	TCTTTGCTGG	TTCCCTCTTC	ATTTAAGCCG	TATATTGAAG	AAAAGTGTGT	ATAACGAGAT
	GGACAAGAAC	CGATGTGAAT	TACTTAGTTT	CTTACTGCTC	ATGGATTACA	TCGGTATTAA	CTTGGCAACC
	ATGAATTCAT	GTATAAACCC	CATAGCTCTG	TATTTTGTGA	GCAAGAAATT	TAAAAATTGT	TTCCAGTCAT
	GCCTCTGCTG	CTGCTGTTAC	CAGTCCAAAA	GTCTGATGAC	CTCGGTCCCC	ATGAACGGAA	CAAGCATCCA
	GTGGAAGAAC	CACGATCAAA	ACAACCACAA	CACAGACCGG	AGCAGCCATA	AGGACAGCAT	GAAGTACCA
40	CCCTTAGAAG	CACTCCTCGG	TACTCCCAT	ATCCTCTCGG	AGAAAAAAT	CACAAGGCAA	CTGTGAGTCC
	GGGAATCTCT	TCTCTGATCC	TTCTTCCTTA	ATTCACCTCC	ACACCCAAGA	AGAAATGCTT	TCCAAAAACCG
	CAAGGGTAGA	CTGGTTTATC	CACCCACAAC	ATCTACGAAT	CGTACTTCTT	TAATTGATCT	AATTACATA
	TTCTGCGTGT	TGTATTCAGC	ACTAAAAAAT	GGTGGGAGCT	GGGGGAGAAT	GAAGACTGTT	AAATGAAACC
	AGAAGGATAT	TTACTACTTT	TGCATGAAAA	TAGAGCTTTC	AAGTACATGG	CTAGCTTTTA	TGGCAGTTCT
45	GGTGAATGTT	CAATGGGAAC	TGGTCACCAT	GAACTTTAG	AGATTAACGA	CAAGATTTTC	TACTTTTTTT
	AAGTGATTTT	TTTGTCTTTC	AGCCAAACAC	AATATGGGCT	CAAGTCACTT	TTATTTGAAA	TGTCATTTGG
	TGCCAGTATC	CCGAATTC	GAATTCGGGA	AAAAGTGAAG	GTGTAAAAGC	AGCACAAGTG	CAATAAGAGA
	TATTTCTCTA	AATTTGCCTC	AAGATGGAAA	CCCTTTCCTC	CAGGGCATCC	TTTTGGCTGG	CACTGGTTGG
	ATGTGTAATC	AGTGATAATC	CTGAGAGATA	CAGCACAAAT	CTAAGCAATC	ATGTGGATGA	TTTACCACCT
50	TTTCGTGGCA	CAGAGCTCAG	CTTCCTGGTT	ACCACTCATC	AACCCACTAA	TTTGGTCCTA	CCCAGCAATG
	GCTCAATGCA	CAACTATTGC	CCACAGCAGA	CTAAAATTAC	TTCAGCTTTC	AAATACATTA	AACTGTGAT
	ATCTTGTAAT	ATTTTCATCG	TGGGAATGGT	GGGGAATGCA	ACTCTGCTCA	GGATCATTTA	CCAGAACAAA
	TGTATGAGGA	ATGGCCCCAA	CGCGCTGATA	GCCAGCTTTC	CCCTTGGAGA	CCTTATCTAT	GTGGTCATTG
	ATCTGCTAT	CAATCTATTT	AAGCTGCTGC	CTGCGGCTTC	GGGCTTTC		

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TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT
TACTTAGTTT CTTACTGCTC ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC
CATAGCTCTG TATTTTGTGA GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC
CAGTCCAAAA GTCTGATGAC CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA
ACAACCACAA CACAGACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG
TACTCCATA ATCCTCTCGG AGAAAAAAT CACAAGGCAA CTGTGAGTCC GGAATCTCT TCTCTGATCC
TTCTTCCTTA ATTCACTCCC ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC
CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTACATA TTCTGCGTGT TGTATTCAGC
ACTAAAAAAT GGTGGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT
TGCATGAAAA TAGAGCTTTC AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC
TGGTCACCAT GAAACTTTAG AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC
AGCCAAACAC AATATGGGCT CAAGTCACTT TTATTGAAA TGTCATTGG TGCCAGTATC CCGAATTC-3' (FRAG.
NO: __) (SEQ ID NO: 3014)
5'-GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTCCTCA AATTGCGCTC
AAGATGGAAG CCCTTTCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC
CTGAGAGATA CAGCACAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG
CTTCCTGGTT ACCACTCATC AACCCTACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC
CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTGTACT ATTTTCATCG
TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT
AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCTT
TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTGACA GGTACAGAGC
AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCTT TTGGTAACTG CCATTGAAAT TGTCTCCATC
TGGATCCTGT CCTTTATCCT GGCCATTCTT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG
GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA
CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT
TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG
AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG
TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC
ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA
GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC
CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG
AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCATA ATCCTCTCGG
AGAAAAAAT CACAAGGCAA CTGTGAGTCC GGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCACTCCC
ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT
CGTACTTCTT TAATTGATCT AATTACATA TTCTGCGTGT TGTATTACAGC ACTAAAAAAT GGTGGGAGCT
GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC
AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG
AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT
CAAGTCACTT TTATTGAAA TGTCATTGG TGCCAGTATC CCGAATTC-3' (FRAG. NO: __) (SEQ ID NO: 2482)
5'-GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTCCTCA AATTGCGCTC
AAGATGGAAG CCCTTTCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC
CTGAGAGATA CAGCACAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG
CTTCCTGGTT ACCACTCATC AACCCTACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC
CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTGTACT ATTTTCATCG
TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT
AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCTT
TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTGACA GGTACAGAGC
AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCTT TTGGTAACTG CCATTGAAAT TGTCTCCATC
TGGATCCTGT CCTTTATCCT GGCCATTCTT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG
GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA
CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT
TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG
AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG
TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC
ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA
GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC
CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG
AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTTAGAAG CACTCCTCGG TACTCCATA ATCCTCTCGG
AGAAAAAAT CACAAGGCAA CTGTGAGTCC GGAATCTCT TCTCTGATCC TTCTTCCTTA ATTCACTCCC
ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT
CGTACTTCTT TAATTGATCT AATTACATA TTCTGCGTGT TGTATTACAGC ACTAAAAAAT GGTGGGAGCT
GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTTT TGCATGAAAA TAGAGCTTTC
AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG
AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT
CAAGTCACTT TTATTGAAA TGTCATTGG TGCCAGTATC CCGAATTC-3' (FRAG. NO: __) (SEQ ID NO: 2482)
5'-GAATTCGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTCCTCA AATTGCGCTC
AAGATGGAAG CCCTTTCCT CAGGGCATCC TTTTGGCTGG CACTGGTTGG ATGTGTAATC AGTGATAATC
CTGAGAGATA CAGCACAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTTCGTGGCA CAGAGCTCAG
CTTCCTGGTT ACCACTCATC AACCCTACTAA TTTGGTCCTA CCCAGCAATG GCTCAATGCA CAACTATTGC
CCACAGCAGA CTAAAATTAC TTCAGCTTTC AAATACATTA ACACTGTGAT ATCTGTACT ATTTTCATCG
TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTTA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT
AAGCTGCTGG CTGGGCGCTG GCCTTTTGAT CACAATGACT TTGGCGTATT TCTTTGCAAG CTGTTCCCTT
TTTTGCAGAA GTCCTCGGTG GGGATCACCG TCCTCAACCT CTGCGCTCTT AGTGTGACA GGTACAGAGC
AGTTGCCTCC TGGAGTCGTG TTCAGGGAAT TGGGATTCTT TTGGTAACTG CCATTGAAAT TGTCTCCATC
TGGATCCTGT CCTTTATCCT GGCCATTCTT GAAGCGATTG GCTTCGTCAT GGTACCCTTT GAATATAGGG
GTGAACAGCA TAAAACCTGT ATGCTCAATG CCACATCAAA ATTCATGGAG TTCTACCAAG ATGTAAAGGA
CTGGTGGCTC TTCGGGTTCT ATTTCTGTAT GCCCTTGGTG TGCACTGCGA TCTTCTACAC CCTCATGACT
TGTGAGATGT TGAACAGAAG GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG
AAGTGGCAAA AACAGTTTTC TGCTTGGTTG TAATTTTGC TCTTTGCTGG TTCCCTCTTC ATTTAAGCCG
TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC
ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTTGTGA
GCAAGAAATT TAAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA GTCTGATGAC
CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAAA ACAACCACAA CACAGACCGG

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CGTACTTCTT TAATTGATCT AATTTACATA TTCTGCGTGT TGTATTCAGC ACTAAAAAAT GGTGGGAGCT
 GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTAATACTTT TGCATGAAAA TAGAGCTTTT
 AAGTACATGG CTAGCTTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG
 AGATTAACGA CAAGATTTTC TACTTTTTTT AAGTGATTTT TTTGTCCTTC AGCCAAACAC AATATGGGCT
 5 CAAGTCACTT TTATTGAAA TGTCATTTGG TGCCAGTATC CCGAATTC-3' (FRAG. NO: __) (SEQ ID NO: 2470)
 5'-GCCACCATGG AAACCTTTG CCTCAGGGCA TCCTTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA
 ATCTGAGAG ATACAGCACA AATCTAAGCA ATCATGTGGA TGATTTTACC ACTTTTCGTG GCACAGAGCT
 CAGCTTCTG GTTACCACTC ATCAACCCAC TAATTTGGTC CTACCCAGCA ATGGCTCAAT GCACAACTAT
 TGCCACAGC AGACTAAAAT TACTTCAGCT TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTTCA
 10 TCGTGGGAAT GGTGGGGAAT GCAACTCTGC TCAGGATCAT TTACCAGAAC AAATGTATGA GGAATGGCCC
 CAACGCGCTG ATAGCCAGTC TTGCCCTTGG AGACCTTATC TATGTGGTCA TTGATCTCCC TATCAATGTA
 TGGCTGGGCG CTGGCCTTTT GATCACAATG ACTTTGGCGT ATTCTTTTGC AAGCTGTTC CTTTTTTC
 GAAGTCCTCG GTGGGGATCA CCGTCCTCAA CCTCTGCGCT CTTAGTGTG ACAGGTACAG AGCAGTTGCC
 TCCTGGAGTC GTGTTCAAGG AATTGGGATT CCTTTGGTAA CTGCCATTGA AATTGCCTCC ATCTGGATCC
 15 TGTCCTTAT CCTGGCCATT CCTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA
 GCATAAAACC TGTATGCTCA ATGCCACATC AAAATTTCATG GAGTTCTACC AAGATGTAAA GGAAGTGGG
 CTCTTCGGGT TCTATTTCTG TATGCCCTTG GTGTGCACTG CGATCTTCTA CACCCTCATG ACTGGTGAGA
 TGTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG TGAACATCTT AAGCAGCGTC GAGAAGTGGC
 AAAACAGTT TTCTGCTTGG TTGTAATTTT TGCTCTTTGC TGGTTCCCTC TTCATTTAAG CCGTATATTG
 20 AAGAAAACCTG TGTATAACGA GATGGACAAG AACCGATGTG AATTACTTAG TTTCTTACTG CTCATGGATT
 ACATCGGTAT TAACTTGGCA ACCATGAATT CATGTATAAA CCCCATAGCT CTGTATTTTG TGAGCAAGAA
 ATTTAAAAAT TGTTCCAGT CATGCCTCTG CTGCTGCTGT TACCAGTCCA AAAGTCTGAT GACCTCGGTC
 CCCATGAACG GAACAAGCAT CCAGTGGAAG AACCACGATC AAAACAACCA CAACACAGAC CGGAGCAGCC
 ATAAGGACAG CATGAACTGA CCACCCTTAG AAGCACTCCT-3' (FRAG. NO: __) (SEQ ID NO: 2469)

- 25 **Substance P Antisense Nucleic Acids and Oligonucleotide Antisense Oligonucleotide Fragments**
 5'-CTGCTGBGGC TTGGGTCTCC GGGCGBTTCT CTGCBGBBGB TGCTCBBBGG GCTCCGGCBG TTCCTCCTTG
 BTCTGGTCGCT GTCGTBCCBG TCGGBCCBG BBTTCBGBTC BTCBTGGCT CCTBTCTCTT CTGCBBCBG
 CTGBGTGBG BCBBGBBBB BGBCTGCCBB GGCCBCGBGG BTTTTCBTGT TGGBTTTTGC GBCGBCBG
 CCCGCGGGGT GCTGAGTTTC TCTGGTTCCT CCGBGCGBCB GTGGTCGCTC CGCGTTTCTC TGGTTCCTCC
 30 GGTCCCGCGG GGTGCTGTCT GGTGCTGTG GTGGCTGGG TCTCCGGGCG GTTCTCTTCC TTTCCGC-3' (FRAG.
 NO:1877) (SEQ ID NO: 1890)
 5'-CTCC GGGCGB-3' (FRAG. NO:1878) (SEQ ID NO: 1891)
 5'-GGCCBCGBGG-3' (FRAG. NO:1879) (SEQ ID NO: 1892)
 5'-GGGTCTCCGGGCG-3' (FRAG. NO:1880) (SEQ ID NO: 1893)
 35 5'-GGG TCTCCGGGCG G-3' (FRAG. NO:1881) (SEQ ID NO:1894)
 5'-CGTGGTCGCTCCGC-3' (FRAG. NO:1355)(SEQ. ID NO:1364)
 5'-GTTTCTCTGGTTCCTCCG-3' (FRAG. NO:1356)(SEQ. ID NO:1365)
 5'-GTCCCGCGGGGTGCTG-3' (FRAG. NO:1357)(SEQ. ID NO:1366)
 5'-TCTGGTCGCTGTCGT-3' (FRAG. NO:1358)(SEQ. ID NO:1367)
 40 5'-GGCTTGGGTCTCCGGGCG-3' (FRAG. NO:1359)(SEQ. ID NO:1368)
 5'-GTTTCTCTCTTTTCCGC-3' (FRAG. NO:1360)(SEQ. ID NO:1369)
 5'-CTGCTGBGGC TTGGGTCTCC GGGCGBTTCT CTGCBGBBGB TGCTCBBBGG GCTCCGGCBG TTCCTCCTTG
 BTCTGGTCGCT GTCGTBCCBG TCGGBCCBG BBTTCBGBTC BTCBTGGCT CCTBTCTCTT CTGCBBCBG
 CTGBGTGBG BCBBGBBBB BGBCTGCCBB GGCCBCGBGG BTTTTCBTGT TGGBTTTTGC GBCGBCBG
 45 CCCGCGGGGT GCTGAGTTTC TCTGGTTCCT CCGBGCGB-3' (FRAG. NO:1882) (SEQ ID NO: 1895)

Substance P Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-GGGCTBBGBT GBTCCBCBTC BCTBCCBCGT TGCCCBCCBC BGBGGTCBCC BCBTGBCCG TGTBGGCBGC
 TGCCBBBGG BCBTBTGCC BGGCTGGTTG CBCGBBCTGB TTGGGTTCG BGGTGTBGT GGBGTGTTT
 GGGGBBGGT CTGBGTCCBC CGGGBGGBCG TTBTCBTTT CGBBGCTBGG CGGTBBBGCC CTBCTBTCTG
 50 TBCBCBCCC CCCTCTGCBG CBGBGTCTG TCGTGGCGCC TGGGGCTCBG GGTCGGGC TAAGATGATC
 CACATCACTA CCACGTTGCC CACCACAGAG GTCACCACAA TGACCGTGTA GGCAGCTGCC CAAAGGACAA
 TTTGCCAGG TGGTTGCACG AACTGATTGG GTTCCGAGGT GTTAGTGGAG ATGTTTGGG AGAGGTCTGA
 GTCCACCGG AGGACGTTAT CCATTCGAA GCTAGGCGGT AAAGCCCTAC TATCTGTACA CAACCCCTT
 CTGCAGCAGA GTCCTGTCGT GGCGCTGGG GCTCAGGGTC CGTCCTGTCG TGGCGCCTGG GGCTCTTCTT
 55 TTGTGGGCTC TTTGGTGGCT GTGGCTGTG TCTCTGTGGT TGCTGCCCTG GGTCTGGGGG TGTGGCCTTG
 GGGCCGTCCT CTGGCTCCTC CTCGTGGGCC CCC-3' (FRAG. NO:1883) (SEQ. ID NO:1896)
 5'-GGGBGGBCG-3' (FRAG. NO:1884) (SEQ. ID NO:1897)
 5'-GGGTC CG-3' (FRAG. NO:1885) (SEQ. ID NO:1898)
 5'-GGGCC CCC-3' (FRAG. NO:1886) (SEQ. ID NO:1899)

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5'-TTCTTTTGTGGGCT-3' (FRAG. NO:1362)(SEQ. ID NO:1371)

5'-CTTTGGTGGCTGTGGCTG-3' (FRAG. NO:1363)(SEQ. ID NO:1372)

5'-TGGTCTCTGTGGTTG-3' (FRAG. NO:1364)(SEQ. ID NO:1373)

5'-CTGCCCTGGGTCTGG-3' (FRAG. NO:1365)(SEQ. ID NO:1374)

5'-GGGTGTGGCCTTGGGGCCGTCCTCTGGCTCCTCCTCGTGGGCCCC (FRAG.NO:1366)(SEQ.ID NO:1375)

5'-GGGCTAAGAT GATCCACATC ACTACCAGT TGCCACCAC AGAGGTCACC ACAATGACCG TGTAGGCAGC
TGCCCAAAGG ACAATTGCC AGGCTGGTTG CACGAACTGA TTGGGTCCG AGGTGTTAGT GGAGATGTTT
GGGGAGAGGT CTGAGTCCAC CGGGAGGACG TTATCCATTTC GAAGCTAGGC GGTAAAGCCC TACTATCTGTA
CACAACCCCC CTCTGCAGCA GAGTCCTGTC GTGGCGCCTG GGGCTCAGGGTCC-3' (FRAG.NO:1367)(SEQ.ID NO:1376)

10 5'-GGGCTBBGBT GBTCCBCBTC BCTBCCBCGT TGCCCBCCBC BGBGGTCBCC BCBTGBCCG TGTBGGCBGC
TGCCBBBGG BCBTTTGCC BGGCTGGTTG CBCGBBCTGB TTGGGTCCG BGGTGTBTGT GGBGBTGTTT
GGGBBGGGTC TGBGTCCBCC GGBBGGBCGT TBTCCBTTC GBBGCTBGGC GGTBBBCCCC TBCTBTCTGTB
CBCBCCCC CTCTGCBGCB GBGTCTGTC GTGGCGCCTG GGGCTCBGGG TCC-3' (FRAG. NO:1368) (SEQ. ID NO:1377)

Chymase Antisense Nucleic Acids and Oligonucleotides Antisense Oligonucleotide Fragments

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 TACTTTGTGA CTTTCTCACT CTGTGACCAT GCTCAAGAGC TATGGAGAAA TCTAAAACAG GAACCTGGAC
 55 AGTGGGTCTT ACACAGAGAC AGAGGAGAGT GGGCCAGGGC AAGGTGGGAG TGGGAGAAGT CTGAGATGAA
 AACATCAGAA TGGAGCAGAG GCAAGAATGA GATTTACCT GGGAGGTTAT GGGTGGGAA AGATACGAAA
 TACAGGAGAC AGGAGAGGGA AGATGGGCGG AACACAGGGT GAGAATGAGA TTCCAGGGAA GCCTAGCTCA
 GCTTTAACC CATTGTCCA TTCAATTGGAG AGAGTATCTA TGGCCGTGTT CAAACCCTGG GGTGCTCTGT
 TCCAGGGGAG ATCATCGGGG GCACAGAATG CAAGGCCAT TCCCGCCCT ACATGGCCTA CCTGGAAATT
 60 GTAACCTCCA ACGGTCCCTC AAAATTTTGT GGTGCTTTCC TTATAAGACG GAACCTTTGTG CTGACGGCTG
 CTCATTGTGC AGGAAGGTGA GACAACAGGG TCTATTTATC TCCAAATGGG AGATGAACAA CCAGAGTAGC
 ATCCAGGAAT ACACCTGCAC TGGGGACTGA AGAGGGGGTC CTGGGTCTTG TCAACTTTCA GGAGAGGGAA

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GACTTTGGGC TGAAAGACTT TAGTCTGTGT TTGAATAGTT CCTTGAGCCT CAGTCACTGA GCTAAGCTCC
CTTCGGAGGA AAAGGAGGTC CTGTCCGAAG GTCCCTCTTG TTGCAGTAGC ACCCCTCACC CCTACCCAAC
TCAAGACACA CGGCTCACTT TTCAGGGCCC CACCCAGTCT CAGGGCCACT TCCTCTATGG CCTTTTCAAG
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5 CCCCCACTTT CCCGTTTAA CTGATATCTC CTGCTTCAGG GGCTGGCCCT CATGCAGGGT TCCCTGAATT
AGGAAGTGTG AACCTGTCC CTGAGTCCT CCCTGGCCTG TTCAGTCCCC AGCAATTCCA GGGGTCGTAG
AAATTGTGTC TGTTTCTGA GAAAGCTCTT TCATGAGTTA AGCCTGAGCC CTCAAATGCC ACAAGTGGCC
CATGAAAAGG GAGATGGGTA GAGTCCGGCN ACCCAGTGAC AGAGTTTAGT CCTCTTTTCT CAGAATGAGC
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10 TAACAGTCAC CTTGGAGCC CATAACATAA CAGAGGAAGA AGACACATGG CAGAAGCTTG AGGTTATAAA
GCAATTCGT CATCCAAAAT ATAACACTTC TACTCTTAC CACGATATCA TGTTACTAAA GGTGACAACA
CCTCTCTTCT CCCTTTCCAC TTCCATTCT CTAAGCTTC TCCTTCAGGT CCTCATTGCC CTGAATTTT
CTTAGGACTT GGCTATAACA TGAAGCTACT CACCCTGTCC CTCCCTGATC ACCTCCAAC GTCCAGAGCC
CATTCGAGG ACTGACAGTC CTTCATTCCC TTCACAGTTG AAGGAGAAAG CCAGCCTGAC CCTGGCTGTG
15 GGGACACTCC CTTCCCATC ACAATTCAAC TTTGTCCAC CTGGGAGAAT GTGCCGGGTG GCTGGCTGGG
GAAGAACAGG TGTGTTGAAG CCGGGCTCAG ACACTCTGCA AGAGGTGAAG CTGAGACTCA TGGATCCCCA
GGCCTGCAGC CACTTCAGAG ACTTTGACCA CAATCTTCAG CTGTGTGTGG GCAATCCCAG GAAGACAAAA
TCTGCATTTA AGGTGATCCT CCAACTAGGT TTCCTCTCCA AAACACTG TTCAGGGACC TGAATGTCT
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20 CGTGGTCCAA GACAGCCTCT GACCATCCAT TCCAGTCTAC TGCCTGGGG GCATGGGGTG ACTGTGGAGA
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25 CGGCCCTGGA TCAACCAGAT CCTGCAGGCA AATTAATCCT GGATCCTGAG CCAGCCTGAA GGAAGCTGG
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CGTGAGTGTG TGTCCTCTC TGCTGTCTC TTCTCCTGCA CATGTGACCT GATTCCCAGC CCAAGCACA AGGA-3'
(FRAG. NO:) (SEQ. ID NO:2467)
30 5'-GGBGCBBCB-3' (FRAG. NO:1888) (SEQ. ID NO:1901)
5'-GGBGCBGC-3' (FRAG. NO:1889) (SEQ. ID NO:1902)
5'-GGGCBBCG CG-3' (FRAG. NO:1890) (SEQ. ID NO:1903)
5'-CGTTTTCTCTCTC-3' (FRAG. NO:1369)(SEQ. ID NO:1378)
5'-GCTGGTTTTCTTTCC-3' (FRAG. NO:1370)(SEQ. ID NO:1379)
35 5'-TGGCAGTGGGTGGGGTGGGGTGGGGTGGC-3' (FRAG. NO:1371)(SEQ. ID NO:1380)
5'-TTCTTGTCTCTGGGGTGTCT-3' (FRAG. NO:1372)(SEQ. ID NO:1381)
5'-CTTGCTCTGGGCTTTTCT-3' (FRAG. NO:1373)(SEQ. ID NO:1382)
5'-CCCCTTTTCTTCC-3' (FRAG. NO:1374)(SEQ. ID NO:1383) [
5'-TGCTGTTTTCTGGGG-3' (FRAG. NO:1375)(SEQ. ID NO:1384)
40 5'-CTCTCCTCTGCTCTGTGT-3' (FRAG. NO:1376)(SEQ. ID NO:1385)
5'-CCTTGCCCTGGCCC-3' (FRAG. NO:1377)(SEQ. ID NO:1386)
5'-TCTTCCCTCTCTGTCTCTGT-3' (FRAG. NO:1378)(SEQ. ID NO:1387)
5'-CCCTGTGTCCGCCC-3' (FRAG. NO:1379)(SEQ. ID NO:1388)
5'-GTCTTCCCTCTCTGT-3' (FRAG. NO:1380)(SEQ. ID NO:1389)
45 5'-ACCTCCTTTCTCTCCG-3' (FRAG. NO:1381)(SEQ. ID NO:1390)
5'-CTGGGTGGGGCCCTG-3' (FRAG. NO:1382)(SEQ. ID NO:1391)
5'-CCTGTTCTCTGTCCC-3' (FRAG. NO:1383)(SEQ. ID NO:1392)
5'-TGGCTTGGGGTTTCTCTG-3' (FRAG. NO:1384)(SEQ. ID NO:1393)
5'-TGTGTCTTCTCTCTGTT-3' (FRAG. NO:1385)(SEQ. ID NO:1394)
50 5'-GGCTGGCTTCTCTCTC-3' (FRAG. NO:1386)(SEQ. ID NO:1395)
5'-TTTTGTCTCTCTGGG-3' (FRAG. NO:1387)(SEQ. ID NO:1396) [1397]]
5'-TGCCCCCTTCTCTTCTTGGG-3' (FRAG. NO:1388)(SEQ. ID NO:1397)
5'-TCCTTGGTGCTTGGGCTGGG-3' (FRAG. NO:1389)(SEQ. ID NO:1398)
5'-GGBGCTGBTB CTGCBGATTT CBGBGGGBBG BBCCCTGBTB CTCBCCBGCT TCBGCTCTGG BGCBCBBGBG
55 BBBGBGCBGC BGGGGGBBG GBBGBGCBG CBCTTCCCB GBGBGGCTGC CTGBGCBBBT GCTGGTTTTT
CTTCCBGTC TTGGGTTTTB TBBCTCCCBG BBGGCBGBG BGGGGCBGG-3' (FRAG. NO:1891) (SEQ. ID NO:1904)

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	GCCGTCCTGC	TGCCGGTCGT	TGGCTGGGTC	CCCCCGCCCG	TTTCCTGGGG	TCCGCGTGGG	GTGCTCCGGT
	TCCTCGTGCC	GCTGCTGCCT	TGTCTTTCCG	GCCGTGGCGG	CGTGGTGGTC	CGCCCCCCT	GGCCTTCTGC
	TCGGGGTCTG	GCTGGTTGCC	GGTGCCCTTG	GCGGCGGTCT	TCTTCCTGGT	GGCTCTGGGC	CCGGCCGGTC
	TCGGGCGTCT	CGTGTTGCT	CTTGTTGCTGT	TCCGGCCGCT	CCTTCCTCTT	CGCCCGCCGC	CGCTCCCCGC
5	CCGCTCGTCG	CCCTGGCCCC	GCCTCCTCCT	GGCCGCTGTC	TCGGGCGGGC	GCCTTGGCGC	TCCGTTTGGG
	GCTGCCTCTG	GCGCTTCCGG	CCCTCGGCCT	GGGCGCTCTC	TTCCGCCTGT	GCTGGTGGCC	CTCGTGGGCC
	CCTCTGGGCC	TCCGGTGTCC	TGTGGTCCCC	CGGCTGGTGG	CCGGGCCGGT	TGGGCGGGCG	TGGGCGCCGG
	CGGGTCCCTC	GGGCTGCCCT	TCTCCGCCGG	GGGTCCCGCG	CTCCTGCTGT	TCCCTGGGCT	CTTCTGCCTC
	TCTCCTGGGT	GGGTGCTGGG	TGCCGGGGTC	TCCGGGCTTG	CCCCGCGCTG	CTGGGCGTTC	TGCGGTCTTG
10	GGGTTGTCTG	TGGCCCCGCT	CGTGTCGCCC	TCCGTCGCCC	GTCGCCGGCC	TCGTCCCCTC	CTGGGTGCGC
	GGCGGGCTGG	TCCTGGCGTT	TTGCTCCTTC	CTGGGCGTCT	TGGGGTGCBG	GGCCCBCTCT	GCTGCGCCTG
	GGCGCTGCTG	TGCGTCCGTC	TGCTGGGGGG	CCGGGGTGGC	TGGGCCCTGC	TTGCCGCACG	ACCCCGGGCC
	GACCCGAGGC	TCGGGGGGCT	GTGTTCTGGC	GCTGGTGGGC	TTGGGCCCTT	CTGGGGGCTG	GGTTTCTCTG
	TGCGCCTGGG	CGCTGGCGTC	TTGGGGTGGC	GGGCCGGGGG	GCCGGGGGGC	CGCTGTTCTG	GGGCCTGGGG
15	GTGCTGTGG	CTGCCGGTTG	CCCCGGTTGG	TGGCGCCGTC	CTGCTGCCGG	TCGTTGGCTG	GGTCCCCCGG
	CCCGTTTCCT	GGGGTCCGCG	TGGGGTGTCT	CGTTCTCTCG	TGCCGCTGCT	GCCTTGTCTT	TCCGGCCGTG
	GCGGCGTGGT	GGTCCGCCCC	CCCTGGCCTT	CTGCTCGGGG	TCTGGCTGGT	TGCCGGTGCC	CTTGGCGGCG
	GTCTTCTTCC	TGGTGGCTCT	GGGCCCCGCC	GGTCTCGGGC	GTCTCGTGT	CGCTCTGTG	CTGTTCCGGC
	CGTCTCTTCC	TCTTCCGCCG	CCGCCGCTCC	CCGCCGCTC	GTCGCCCTGG	CCCGGCCTCC	TCCTGGCCGC
20	TGTCTCGGGC	GGCGGCCTTG	GCGCTCCGTT	TGGGGCTGCC	TCTGGCGCTT	CCGGCCCTCG	GCCTGGGCGC
	TCTCTCCGCG	CTGTGCTGGT	GGCCCTCGTG	GGCCCTCCT	GGCCTCCGGT	GTCTGTGGT	CCCCCGGCTG
	GTGGCCGGGC	CGGTTGGGCG	GGCGTGGGCG	CCGGCGGGTC	CTCCGGGCTG	CCCTTCTCCG	CCGGGGGTCC
	CGCGTCTCTG	CTGTTCCCTG	GGCTCTTCTG	CCTCTCTCCT	GGGTGGGTGC	TGGGTGCCGG	GGTCTCCGGG
	CTTGCCCCCG	GCTGCTGGGC	GTTCTGCGGT	CTTGGGGTTG	TCTGTGGCCC	CGCTCGTGTC	GCCCTCCGTC
25	GCCCCGCTCC	GGCCTCGTCC	CCTCCTGGGT	GCGCGCGGG	CTGGTCTGG	CGTTTGTCTC	CTTCTGG-3' (FRAG.
	NO:1892) (SEQ. ID NO: 1905)						
	5'-GCGGGGCCG-3' (FRAG. NO:1893) (SEQ. ID NO: 1906)						
	5'-CGGGGGGC-3' (FRAG. NO:1894) (SEQ. ID NO: 1907)						
	5'-GCGCGCGGGC-3' (FRAG. NO:1895) (SEQ. ID NO: 1908)						
30	5'-CTGTGCGTCCGTCGCTGG (FRAG. NO:1390)(SEQ. ID NO:1399)						
	GGGGCCGGGGTGGCTGGGCCCTGCTTGCCG (FRAG. NO:1391)(SEQ. ID NO:1400)						
	ACGACCCCGGGCCGACCCGAG (FRAG. NO:1392)(SEQ. ID NO:1401)						
	GCTCGGGGGGCTGTGTTCTGGCGCTGGTGGG (FRAG. NO:1393)(SEQ. ID NO:1402)						
	CTTGGGCCCCCTCTGGGGGCTGGGTT (FRAG. NO:1394)(SEQ. ID NO:1403)						
35	TCCTGCTGCGCCTGGGCGCTG (FRAG. NO:1395)(SEQ. ID NO:1404)						
	GCGTCTTGGGGTGC (FRAG. NO:1396)(SEQ. ID NO:1405)						
	GGGGCCGGGGGCGGGG (FRAG. NO:1397)(SEQ. ID NO:1406)						
	GCCGCTGTTCTGTGGCCTGGG (FRAG. NO:1398)(SEQ. ID NO:1407)						
	GGTGCTGTGGCTGCC (FRAG. NO:1399)(SEQ. ID NO:1408)						
40	GGTTGCCCCGGTTGGTGGC (FRAG. NO:1400)(SEQ. ID NO:1409)						
	GCCGCTCTGCTGCCGT (FRAG. NO:1401)(SEQ. ID NO:1410)						
	CGTTGGCTGGGTCCCCCGC (FRAG. NO:1402)(SEQ. ID NO:1411)						
	CCGTTTCTGGGGTCC (FRAG. NO:1403)(SEQ. ID NO:1412)						
	GCGTGGGGTGTCTC (FRAG. NO:1404)(SEQ. ID NO:1413)						
45	GGTTCTCTGTGCCG (FRAG. NO:1405)(SEQ. ID NO:1414)						
	CTGCTGCCTTGTCTTCC (FRAG. NO:1406)(SEQ. ID NO:1415)						
	GGCCGTGGCGGCGTGGTGGTCC (FRAG. NO:1407)(SEQ. ID NO:1416)						
	GCCCCCCTGGCCTTCTGCTC (FRAG. NO:1408)(SEQ. ID NO:1417)						
	GGGGTCTGGCTGGT (FRAG. NO:1409)(SEQ. ID NO:1418)						
50	TGCCGGTGCCCTTGGCGGC (FRAG. NO:1410)(SEQ. ID NO:1419)						
	GGTCTTCTTCTCTGGTG (FRAG. NO:1411)(SEQ. ID NO:1420)						
	GCTCTGGGCGCGCGGTCTCGG (FRAG. NO:1412)(SEQ. ID NO:1421)						
	GCGTCTCGTGTTCG (FRAG. NO:1413)(SEQ. ID NO:1422)						
	CTCTGTGCTGTTCGGCCG (FRAG. NO:1414)(SEQ. ID NO:1423)						
55	CTCCTTCTCTTCCGCCGCC (FRAG. NO:1415)(SEQ. ID NO:1424)						
	GCCGCTCCCCGCC (FRAG. NO:1416)(SEQ. ID NO:1425)						
	GCTCGTCGCCCTGGCCC (FRAG. NO:1417)(SEQ. ID NO:1426)						
	GGCCTCCTCTGGCCGC (FRAG. NO:1418)(SEQ. ID NO:1427)						
	TGCTCGGGCGGCGCCTTGGC (FRAG. NO:1419)(SEQ. ID NO:1428)						
60	GCTCCGTTTGGGGCTG (FRAG. NO:1420)(SEQ. ID NO:1429)						
	CCTCTGGCGCTTCC (FRAG. NO:1421)(SEQ. ID NO:1430)						
	GGCCCTCGGCTGGGCGCTC (FRAG. NO:1422)(SEQ. ID NO:1431)						

- TCTTCCGCCTGTGC (FRAG. NO:1423)(SEQ. ID NO:1432)
 TGGTGGCCCTCGTGG (FRAG. NO:1424)(SEQ. ID NO:1433)
 GCCCCTCTGGCCTCCGGTGTCC (FRAG. NO:1425)(SEQ. ID NO:1434)
 TGTGGTCCCCCGGTGGT (FRAG. NO:1426)(SEQ. ID NO:1435)
 5 GGCCGGGCGCGTTGGGCGGGC (FRAG. NO:1427)(SEQ. ID NO:1436)
 GTGGGCGCGGCGGGTCTCC (FRAG. NO:1428)(SEQ. ID NO:1437)
 GGGCTGCCCTTCTCC (FRAG. NO:1429)(SEQ. ID NO:1438)
 GCGGGGGTCCCGC (FRAG. NO:1430)(SEQ. ID NO:1439)
 GCTCCTGCTGTTCCCTGGGCTCTCTGCC (FRAG. NO:1431)(SEQ. ID NO:1440)
 10 TCTCTCCTGGGTGGGTGCTGGGTGCCG (FRAG. NO:1432)(SEQ. ID NO:1441)
 GGGTCTCCGGGCTTG (FRAG. NO:1433)(SEQ. ID NO:1442)
 CCCCgcgctgctgggCGTTCTGC (FRAG. NO:1434)(SEQ. ID NO:1443)
 GGTCTTGGGGTTGTC (FRAG. NO:1435)(SEQ. ID NO:1444)
 TGTGGCCCCGCTCG (FRAG. NO:1436)(SEQ. ID NO:1445)
 15 TGTCGCCCTCCGTCGCC (FRAG. NO:1437)(SEQ. ID NO:1446)
 CGTCGCCGGCCTCGTCC (FRAG. NO:1438)(SEQ. ID NO:1447)
 CCTCCTGGGTGCGC (FRAG. NO:1439)(SEQ. ID NO:1448)
 GGCGGGCTGGTCCT (FRAG. NO:1440)(SEQ. ID NO:1449)
 GGCGTTTGTCTCCTTCTG (FRAG. NO:1441)(SEQ. ID NO:1450)
 20 5'-GCGTCTTGGGTGCBGGGCCBTCTGCTGCGCCTGGGCGCTG-3' (FRAG. NO:1896) (SEQ. ID NO: 1909)

Inducible Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-CTGCCCCBGT TTTTGBCTCT CBCBTGCCGT GGGGBGGBCB BTGGCTGCCT CCCCggggtt TCTGCTGCTT
 GCTGCTTCTT TCCCGTCTCC CTCTTTTCCC GTCTCCTTTT TGCCCTCTTG GGTTCCTGTT GTTTCTGGCC
 TGCTTGGTGG CGGCTTGTGC GTTCTCTCTC TCTTCTCTTG GGTCTCCGCT TCTCGTCTG CTTTTCCTG
 25 TCTCTGTGCG GCGGTCTCTC CTCCGGCGTC CTCTGCCCT GTGCTGTTG CCTCGGGTGG TGCGGGTCCC
 GGTGCTCCCC CGGCGGGCCG GCTGGTTGCC TGGGCCTGTC TGGTGGGGTG TGGGGCCGCT GGGTTGGGGG
 TGTGGTGGGC TCTTCTGTGG CCTGTGGGGC TGTGGTGTG TCTGTGGGCG TGTGCTGGGT CTTGGGGCTT
 CCTCCCTTGT GCTGGGTGCG GCCTCCCCGC CCCCTTCTG GGCCGGTGGC CTGGCTCCTT GTGGGCGCTT
 CTGGCTCTTG CCCTGTCCTT CTTCGCCCTG TGGCTGCTGG GCTGC CATATGTATG GGAATACTGT ATTTCAAGCA
 30 TTATAAGGAA TGAAATTATA GGCCGGGCAT TGTGGCTAAC CCTTGTAATC CTAGCACTT GAGAGGCTGA
 AGTGGGCAGA TCACTTGAGC TTCAGAGTTC GAGACCAGCA TGGACAACAT GGTGAAACCC AGTCTCTACC
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 GGGAGGATCG CTTGAGCCTG GGAGGCAGAA GTTGCAATGA GCAGAGATCG TGCCACTCCG CTCCAGTCTT
 GGTGACAGAA TGAGACTCCA TCTCAAAAAT AAATAAATAA ATAAATAAAA TAAATGAAAT GAAATTATAA
 35 GAAATTACCA CTTTTTCATG TAAGAAGTGA TCATTTCCAT TATAAGGGAA GGAATTTAAT CCTACCTGCC
 ATTCCACCAA AGCTTACCTA GTGCTAAAGG ATGAGGTGTT AGTAAGACCA ACATCTCAGA GGCCTCTCTG
 TGCCAATAGC CTTCCTTCCT TTCCCTTCCA AAAACCTCAA GTGACTAGTT CAGAGGCCTG TCTGGAATAA
 TGGCATCATC TAATATCACT GGCCTTCTGG AACCTGGGCA TTTTCCAGTG TGTTCATAC TGTCATATT
 CCCCAGCTT CCTGGACTCC TGTCACAAGC TGAAAAAGTG AGAGGATGGA CAGGGATTAA CCAGAGAGCT
 40 CCTGCTGAG GAAAAATCT CCCAGATGCT GAAAGTGAGG CCATGTGGCT TGGCCAAATA AAACCTGGCT
 CCGTGGTGCC TCTGTCTAG CAGCCACCCT GCTGATGAAC TGCCACCTTG GACTTGGGAC CAGAAAGAGG
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 GCTTTAAAAT CTCTCGGCCA CCTTTGATGA GGGGACTGGG CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG
 CACAGGTCTC TTCCTGGTTT GACTGTCCTT ACCCGGGGA GGCAGTGCA CAGCTGCAA GGTGAGTTGC C
 CATATGTATG GGAATACTGT ATTTCAAGCA TTATAAGGAA TGAAATTATA GGCCGGGCAT TGTGGCTAAC
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 50 TGGACAACAT GGTGAAACCC AGTCTCTACC AAAAAACAAA AAATATTAGC TGGGTGTGGT GGTGCAATGC
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 60 TGCCACCTTG GACTTGGGAC CAGAAAGAGG TGGGTGGGT GAAGAGGCAC CACACAGAGT GATGTAACAG
 CAAGATCAGG TCACCCACAG GCCCTGGCAG TCACAGTCAT AAATTAGCTA ACTGTACACA AGCTGGGAC

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ACTCCCTTTG GAAACCAAAA AAAAAAAAAA AAAAAAGAGA CCTTTATGCA AAAACAAC TC TCTGGATGGC
ATGGGGTGAG TATAAATACT TCTTGGCTGC CAGTGTGTTC ATAAC TTGT AGCGAGTCGA AAAGT GAGGC
TCCGGCCGCA GAGAACTCAG CCTCATTCCT GCTTTAAAT CTCTCGGCCA CCTTTGATGA GGGGACTGGG
CAGTTCTAGA CAGTCCCGAA GTTCTCAAGG CACAGGTCTC TTCCTGGTTT GACTGTCCTT ACCCGGGGA
5 GGCAGTGCAG CCAGCTGCAA GGTGAGTTGC C-3' (FRAG. NO:)(SEQ. ID NO: 3016)
5'-CTGCTTTAAA ATCTCTCGGC CACCTTTGAT GAGGGGACTG GGCAGTTCTA GACAGTCCCG AAGTTCTCAA
GGCACAGGTC TCTTCTGGT TTGACTGTCC TTACCCCGGG GAGGCAGTGC AGCCAGTGC AAGCCCCACA
GTGAAGAACA TCTGAGCTCA AATCCAGATA AGTGACATAA GTGACCTGCT TTGTAAAGCC ATAGAGATGG
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10 CAACAATGTG GAGAAAAGCCC CCTGTGCCAC CTCCAGTCCA GTGACACAGG ATGACCTTCA GTATCACAAC
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15 AAGCTATCGA ATTTGTCAAC CAATATTACG GTCCTTCAA AGAGGCAAAA ATAGAGGAAC ATCTGGCCAG
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GCCACCAAGC AGGCCTGGCG CAATGCCCA CGCTGCATTG GGAGGATCCA GTGGTCCAAC CTGCAGGTCT
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25 CACAGAGATC GGAGTCCGGG ACTTCTGTGA CGTCCAGCGC TACAACATCC TGGAGGAAGT GGGCAGGAGA
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35 CTCTTCATGC TGAAAGAGCT CAACAACAAA TTCAGGTACG CTGTGTTTGG CCTCGGCTCC AGCATGTACC
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 AGTGCTACC CCAGCTC-3' (FRAG. NO:_) (SEQ. ID NO:2508)
 5'-CCCCGGGG-3' (FRAG. NO:1898) (SEQ. ID NO:1911)
 15 5'-GGGGCCGCTGGG-3' (FRAG. NO:1899) (SEQ. ID NO:1912)
 5'-GGGGGTGTGG-3' (FRAG. NO:1900) (SEQ. ID NO:1913)
 5'-CTGCCTCCCCGGGT-3' (FRAG. NO:1442)(SEQ. ID NO:1451)
 5'-TTCTGCTGCTTGCTG-3' (FRAG. NO:1443)(SEQ. ID NO:1452)
 5'-CTTCTTTCCCGTCTCC-3' (FRAG. NO:1444)(SEQ. ID NO:1453)
 20 5'-CTTCTTTCCCGTCTCC-3' (FRAG. NO:1445)(SEQ. ID NO:1454)
 5'-TTTTTGCTCTTTG-3' (FRAG. NO:1446)(SEQ. ID NO:1455)
 5'-GGTTCCTGTTGTTTCT-3' (FRAG. NO:1447)(SEQ. ID NO:1456)
 5'-GGCCTGCTTGGTGGCG-3' (FRAG. NO:1448)(SEQ. ID NO:1457)
 5'-GCTTGTGCGTTTCC-3' (FRAG. NO:1449)(SEQ. ID NO:1458)
 25 5'-TCTCTTCTCTTGGGTCTCCGTTCTCGTCTGCC-3' (FRAG. NO:1450)(SEQ. ID NO:1459)
 5'-TTTTCTGTCTCTGTCGC-3' (FRAG. NO:1451)(SEQ. ID NO:1460)
 5'-GCCGTTCCTCCTCC-3' (FRAG. NO:1452)(SEQ. ID NO:1461)
 5'-GGCGTCTCCTGCCC-3' (FRAG. NO:1453)(SEQ. ID NO:1462)
 5'-TGTGCTGTTGCTCGG-3' (FRAG. NO:1454)(SEQ. ID NO:1463)
 30 5'-GTGGTGGGGTCCC-3' (FRAG. NO:1455)(SEQ. ID NO:1464)
 5'-GGTGTCCCCCGGC-3' (FRAG. NO:1456)(SEQ. ID NO:1465)
 5'-GGGCGCGGTGGTGGCCTGGGC-3' (FRAG. NO:1457)(SEQ. ID NO:1466)
 5'-CTGTCTGGTGGGTGGGGGCC-3' (FRAG. NO:1458)(SEQ. ID NO:1467)
 5'-GCTGGGTGGGGGTGTGGTG-3' (FRAG. NO:1459)(SEQ. ID NO:1468)
 35 5'-GGCTCTTCTGTGGCC-3' (FRAG. NO:1460)(SEQ. ID NO:1469)
 5'-TGTGGGGCTGTGGTG-3' (FRAG. NO:1461)(SEQ. ID NO:1470)
 5'-TCTCTGTGGCGTGTG-3' (FRAG. NO:1462)(SEQ. ID NO:1471)
 5'-CTGGGTCTTGGGGCTTC-3' (FRAG. NO:1463)(SEQ. ID NO:1472)
 5'-CTCCCTTGTGCTGGG-3' (FRAG. NO:1464)(SEQ. ID NO:1473)
 40 5'-TGCGGCTCCCCGC-3' (FRAG. NO:1465)(SEQ. ID NO:1474)
 5'-CCCCCTTCTGGGCC-3' (FRAG. NO:1466)(SEQ. ID NO:1475)
 5'-GGTGGCTGGCTCCTGTGG-3' (FRAG. NO:1467)(SEQ. ID NO:1476)
 5'-GCGCTTCTGGCTCTTG-3' (FRAG. NO:1468)(SEQ. ID NO:1477)
 5'-CCCTGTCCTTCTCGCCTCGT-3' (FRAG. NO:1469)(SEQ. ID NO:1478)
 45 5'-GGCTGCTGGGCTGC-3' (FRAG. NO:1470)(SEQ. ID NO:1479)
 5'-CTGCCCCBGTTTTGBTCCTCBCBTGCCGTGGGBGGBCBTGG-3' (FRAG. NO:1901) (SEQ. ID NO:1914)

NF-kB Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-CGGCCCTTCT CACTGGAGGC ACCGGGCACT CCTCCATGGG AGGGTTGGGC TTGGCCGGGG CTGCCCCGGTG
 CCTCCTTTG GCTGGTCCCT CGTTGTCCTT GGGCCCCGC TCCCGCTGCT CGGCCTCCGT GTTCTTTGGC
 50 CTCTGTGCTC GCTGCTGTC TTGTCCCGTC CCCTCCTCGC TTGCGTTTCC CTCTTCCCTG TCTTCCAGGC
 CTCTCTCCGC TTCCGCTGCT GGGGCCCGCG CCGGGGGGGC GCTCGGCTCC GCGGCTTCCCT CCCC GGCTGG
 GGGGTCTGG TCTCCGGGGC CTGCGGCTCG CGGGCTCGGG GCTGCGTGCG CCGCGCGCGG CGTCCGCGGT
 GGGTGGCGCT GTCCCGCCGT GGTGTGTCTC CGTTCTCGTC CTGCGCCGTC CTGGTGTGCC CGTGGGGTCC
 TGGGCGTGGT GGGGGGCGTC TGGTGCCTCG TCTGCCCGT GGGGCTTCGG GCTCGGGCT GTTCGTCCCC
 55 CCTGCCGCTC TGTGGCCTCC GGGGCTCCTC GTTTTCGCTG CTTCGGGTGT CCTTCTCGGC GTGTGGCCCC
 GGGTCCCCGC CCGTGTGGG TGGGCGGGGT CGCTGCCCTG GGCTTCTGGC CCGTCTGGTT GTCTGTCCGT
 GCTTGTCTCG GGTTCCTGGC CTCTGTGCTG GGCGCTTCTC TGCCTCCTGC TCCGCCCTCC TGGTGGCTCG
 GCTGGGGGTG CCCGTGCGGG GGTGGGTGTG GGGTGTTC GGGTCTCTCC CCTTCCC-3' (FRAG. NO:1902) (SEQ.
 ID NO:1915)
 60 5'-GGGCGGGGTGCG-3' (FRAG. NO:1903) (SEQ. ID NO:1916)
 5'-GCGCCGTCC-3' (FRAG. NO:1904) (SEQ. ID NO:1917)

- 5'-GGGCGTGGTGG-3' (FRAG. NO:1905) (SEQ. ID NO:1918)
 5'-GTTGGGCTTGGCCGGG-3' (FRAG. NO:1471)(SEQ. ID NO:1480)
 5'-CTGCCCGGTGCCTCC-3' (FRAG. NO:1472)(SEQ. ID NO:1481)
 5'-TCTTGGCTGGTCCCTCGT-3' (FRAG. NO:1473)(SEQ. ID NO:1482)
 5'-TGTCCTTGGGCCCC-3' (FRAG. NO:1474)(SEQ. ID NO:1483)
 5'-GCTCCCGCTGCTCGGCCCTCCGT-3' (FRAG. NO:1475)(SEQ. ID NO:1484)
 5'-GTTCTTTGGCCTCTTGCTCC-3' (FRAG. NO:1476)(SEQ. ID NO:1485)
 5'-GCCTGTGTCTTGTCC-3' (FRAG. NO:1477)(SEQ. ID NO:1486)
 5'-CGTCCCCCTCGCTTGCGTTTC-3' (FRAG. NO:1478)(SEQ. ID NO:1487)
 5'-CCTCTTCCTTGTCTTCCA-3' (FRAG. NO:1479)(SEQ. ID NO:1488)
 5'-GGCCTTCCTCCGCTTCCGCTGC-3' (FRAG. NO:1480)(SEQ. ID NO:1489)
 5'-TGGGGCCCGCGCCGG-3' (FRAG. NO:1481)(SEQ. ID NO:1490)
 5'-GGGGGCGCTCGGCTCCGCGCTTCTCCCCGG-3' (FRAG. NO:1482)(SEQ. ID NO:1491)
 5'-CTGGGGGCTCTGG-3' (FRAG. NO:1483)(SEQ. ID NO:1492)
 5'-TCTCCGGGGCTGCGGCTCGC-3' (FRAG. NO:1484)(SEQ. ID NO:1493)
 5'-GGGCTCGGGGCTGCGTGCGCC-3' (FRAG. NO:1485)(SEQ. ID NO:1494)
 5'-GCGCGCGGCGTCCGCGGTG-3' (FRAG. NO:1486)(SEQ. ID NO:1495)
 5'-GGTGGCGCTGTCCCGCC-3' (FRAG. NO:1487)(SEQ. ID NO:1496)
 5'-GTGGTGTGTCTCCGTTCTCGTCTGCGCCGTC-3' (FRAG. NO:1488)(SEQ. ID NO:1497)
 5'-CTGGTCTGCCCGTGG-3' (FRAG. NO:1489)(SEQ. ID NO:1498)
 5'-GGTCCTGGGCGTGGTGG-3' (FRAG. NO:1490)(SEQ. ID NO:1499)
 5'-GGGGCGTCTGGTGC-3' (FRAG. NO:1491)(SEQ. ID NO:1500)
 5'-CTCGTCTGCCCCGTG-3' (FRAG. NO:1492)(SEQ. ID NO:1501)
 5'-GGGCTTCGGGCTCGG-3' (FRAG. NO:1493)(SEQ. ID NO:1502)
 5'-GGCTGTCTGTCCTCCCTGCGGCTCTGTGGCCTCC-3' (FRAG. NO:1494)(SEQ. ID NO:1503)
 5'-GGGGCTCCTCGTTTTC-3' (FRAG. NO:1495)(SEQ. ID NO:1504)
 5'-GCTGCTTCGGGTGTCCTTCTC-3' (FRAG. NO:1496)(SEQ. ID NO:1505)
 5'-GGCGTGTGGCCCCGG-3' (FRAG. NO:1497)(SEQ. ID NO:1506)
 5'-GTCCCGGCCCTGCTGGGCTGGGCGGGGTC-3' (FRAG. NO:1498)(SEQ. ID NO:1507)
 5'-GCTGCCCTGGGCTTCTGGCCCGTCT-3' (FRAG. NO:1499)(SEQ. ID NO:1508)
 5'-GGTGTCTGTCTGGT-3' (FRAG. NO:1500)(SEQ. ID NO:1509)
 5'-GCTGTCTCGGGTTTCTGG-3' (FRAG. NO:1501)(SEQ. ID NO:1510)
 5'-CCTCTGTGCTGGGC-3' (FRAG. NO:1502)(SEQ. ID NO:1511)
 5'-GCTTCTCTGCCCTCTGCTCC-3' (FRAG. NO:1503)(SEQ. ID NO:1512)
 5'-GCCCTCTGGTGGGTC-3' (FRAG. NO:1504)(SEQ. ID NO:1513)
 5'-GGCTGGGGGTGCCCCGTGCG-3' (FRAG. NO:1505)(SEQ. ID NO:1514)
 5'-GGGGTGGGTGTGGGTGTT-3' (FRAG. NO:1506)(SEQ. ID NO:1515)
 5'-TTCGGGGTCTCCCTTCCC-3' (FRAG. NO:1507)(SEQ. ID NO:1516)
 5'-CGGCCCTTCTCACTGGAGGACCGGGCAGTCTCCATGGGAGG-3' (FRAG.NO:1906)(SEQ.ID NO:1919)
- 40 **Human Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments**
 5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT
 CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG
 GGA GTT TCA TCT TGG GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG
 TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT
 45 CCC TGC TGG GGG GGB GTT TCB TCT TGG-3' (FRAG. ID:1907) (SEQ. ID NO:1920)
 5'-GGG GGA GTT-3' (FRAG. ID:1908) (SEQ. ID NO:1921)
 5'-G CCC TGG GCC C-3' (FRAG. ID:1909) (SEQ. ID NO:1922)
 5'-GTT TCA TCT TGG CTT TAT CC-3' (FRAG. NO:1508) (SEQ. ID NO:1517)
 5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1509)(SEQ. ID NO:1518)
 50 5'-TCT CCT GCT CTG GRG TCT CCT C-3' (FRAG. NO:1510)(SEQ. ID NO:1519)
 5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1511)(SEQ. ID NO:1520)
 5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1512)(SEQ. ID NO:1521)
 5'-GTT TCG CTC TTG TTG CCC-3' (FRAG. NO:1513)(SEQ. ID NO:1522)
 5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1514)(SEQ. ID NO:1523)
 55 5'-GGG GGA GTT TCA TCT TGG-3' (FRAG. NO:1515)(SEQ. ID NO:1524)
 5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT
 CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG
 GGA GTT TCA TCT TGG GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG
 TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC GTT TCG CTC TTG TTG CCC TGG GCC CTT

Human Eosinophil Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1516)(SEQ. ID NO:1525)
 5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1517)(SEQ. ID NO: 1526)
 5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1518)(SEQ. ID NO:1527)
 5 5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1519)(SEQ. ID NO: 1528)
 5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1520)(SEQ. ID NO: 1529)
 5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1521)(SEQ. ID NO: 1530)
 5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1522)(SEQ. ID NO: 1531)
 5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1523)(SEQ. ID NO: 1532)
 10 5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1524)(SEQ. ID NO: 1533)
 5'-GGG GGB GTT TCB T-3' (FRAG. NO:1525)(SEQ. ID NO: 1534)
 5'-GGG GGB GTT TCB-3' (FRAG. NO:1526)(SEQ. ID NO: 1535)
 5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1527)(SEQ. ID NO: 1536)
 5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1528)(SEQ. ID NO: 1537)
 15 5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1529)(SEQ. ID NO: 1538)
 5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1530)(SEQ. ID NO: 1539)
 5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1531)(SEQ. ID NO: 1540)
 5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1532)(SEQ. ID NO: 1541)
 5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1533)(SEQ. ID NO: 1542)
 20 5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1534)(SEQ. ID NO: 1543)
 5'-GG GGB GTT TCB TC-3' (FRAG. NO:1535)(SEQ. ID NO: 1544)
 5'-GG GGB GTT TCB T-3' (FRAG. NO:1536)(SEQ. ID NO: 1545)
 5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1537)(SEQ. ID NO: 1546)
 5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1538)(SEQ. ID NO: 1547)
 25 5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1539)(SEQ. ID NO: 1548)
 5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1540)(SEQ. ID NO: 1549)
 5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1541)(SEQ. ID NO: 1550)
 5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1542)(SEQ. ID NO: 1551)
 5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1543)(SEQ. ID NO: 1552)
 30 5'-G GGB GTT TCB TCT-3' (FRAG. NO:1544)(SEQ. ID NO: 1553)
 5'-G GGB GTT TCB TC-3' (FRAG. NO:1545)(SEQ. ID NO: 1554)
 5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1546)(SEQ. ID NO: 1555)
 5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1547)(SEQ. ID NO: 1556)
 5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1548)(SEQ. ID NO: 1557)
 35 5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1549)(SEQ. ID NO: 1558)
 5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1550)(SEQ. ID NO: 1559)
 5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1551)(SEQ. ID NO: 1560)
 5'-GGB GTT TCB TCT T-3' (FRAG. NO:1552)(SEQ. ID NO: 1561)
 5'-GGB GTT TCB TCT-3' (FRAG. NO:1553)(SEQ. ID NO: 1562)
 40 5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1554)(SEQ. ID NO: 1563)
 5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1555)(SEQ. ID NO: 1564)
 5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1556)(SEQ. ID NO: 1565)
 5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1557)(SEQ. ID NO: 1566)
 5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1558)(SEQ. ID NO: 1567)
 45 5'-GB GTT TCB TCT TG-3' (FRAG. NO:1559)(SEQ. ID NO: 1568)
 5'-GB GTT TCB TCT T-3' (FRAG. NO:1560)(SEQ. ID NO: 1569)
 5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1561)(SEQ. ID NO: 1570)
 5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1562)(SEQ. ID NO: 1571)
 5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1563)(SEQ. ID NO: 1572)
 50 5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1564)(SEQ. ID NO: 1573)
 5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1565)(SEQ. ID NO: 1574)
 5'-B GTT TCB TCT TGG-3' (FRAG. NO:1565)(SEQ. ID NO: 1575)
 5'-B GTT TCB TCT TG-3' (FRAG. NO:1567)(SEQ. ID NO: 1576)
 5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1568)(SEQ. ID NO: 1577)
 55 5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1569)(SEQ. ID NO: 1578)
 5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1570)(SEQ. ID NO: 1579)
 5'-GTT TCB TCT TGG C-3' (FRAG. NO:1571)(SEQ. ID NO: 1580)
 5'-GTT TCB TCT TGG-3' (FRAG. NO:1572)(SEQ. ID NO: 1581)
 5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1573)(SEQ. ID NO: 1582)
 60 5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1574)(SEQ. ID NO: 1583)
 5'-TT TCB TCT TGG CT-3' (FRAG. NO:1575)(SEQ. ID NO: 1584)

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- 5'-TT TCB TCT TGG C-3' (FRAG. NO:1576)(SEQ. ID NO: 1585)
5'-T TCB TCT TGG CTT T-3' (FRAG. NO:1577)(SEQ. ID NO: 1586)
5'-T TCB TCT TGG CTT-3' (FRAG. NO:1578)(SEQ. ID NO: 1587)
5'-T TCB TCT TGG CT-3' (FRAG. NO:1579)(SEQ. ID NO: 1588)
5 5'-TCB TCT TGG CTT T-3' (FRAG. NO:1580)(SEQ. ID NO: 1589)
5'-TCB TCT TGG CTT-3' (FRAG. NO:1581)(SEQ. ID NO: 1590)
5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1582)(SEQ. ID NO:1591)
5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1583)(SEQ. ID NO: 1592)
5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1584)(SEQ. ID NO: 1593)
10 5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1585)(SEQ. ID NO: 1594)
5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1586)(SEQ. ID NO: 1595)
5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1587)(SEQ. ID NO: 1596)
5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1588)(SEQ. ID NO: 1597)
5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1589)(SEQ. ID NO: 1598)
15 5'-T TCB TCT TGG CTT T-3' (FRAG. NO:1590)(SEQ. ID NO: 1599)
5'-TCB TCT TGG CTT T-3' (FRAG. NO:1591)(SEQ. ID NO: 1600)
5'-CB TCT TGG CTT T-3' (FRAG. NO:1592)(SEQ. ID NO: 1601)
5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1593)(SEQ. ID NO: 1602)
5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1594)(SEQ. ID NO: 1603)
20 5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1595)(SEQ. ID NO: 1604)
5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1596)(SEQ. ID NO: 1605)
5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1597)(SEQ. ID NO: 1606)
5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1598)(SEQ. ID NO: 1607)
5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1599)(SEQ. ID NO: 1608)
25 5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1600)(SEQ. ID NO: 1609)
5'-T TCB TCT TGG CTT-3' (FRAG. NO:1601)(SEQ. ID NO: 1610)
5'-TCB TCT TGG CTT-3' (FRAG. NO:1602)(SEQ. ID NO: 1611)
5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1603)(SEQ. ID NO: 1612)
5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1604)(SEQ. ID NO: 1613)
30 5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1605)(SEQ. ID NO: 1614)
5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1606)(SEQ. ID NO: 1615)
5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1607)(SEQ. ID NO: 1616)
5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1608)(SEQ. ID NO: 1617)
5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1609)(SEQ. ID NO: 1618)
35 5'-TT TCB TCT TGG CT-3' (FRAG. NO:1610)(SEQ. ID NO: 1619)
5'-T TCB TCT TGG CT-3' (FRAG. NO:1611)(SEQ. ID NO: 1620)
5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1612)(SEQ. ID NO: 1621)
5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1613)(SEQ. ID NO: 1622)
5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1614)(SEQ. ID NO: 1623)
40 5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1615)(SEQ. ID NO: 1624)
5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1616)(SEQ. ID NO: 1625)
5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1617)(SEQ. ID NO: 1626)
5'-GTT TCB TCT TGG C-3' (FRAG. NO:1618)(SEQ. ID NO: 1627)
5'-TT TCB TCT TGG C-3' (FRAG. NO:1619)(SEQ. ID NO: 1628)
45 5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1620)(SEQ. ID NO: 1629)
5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1621)(SEQ. ID NO: 1630)
5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1622)(SEQ. ID NO: 1631)
5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1623)(SEQ. ID NO: 1632)
5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1624)(SEQ. ID NO: 1633)
50 5'-B GTT TCB TCT TGG-3' (FRAG. NO:1625)(SEQ. ID NO: 1634)
5'-GTT TCB TCT TGG-3' (FRAG. NO:1626)(SEQ. ID NO: 1635)
5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1627)(SEQ. ID NO: 1636)
5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1628)(SEQ. ID NO: 1637)
5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1629)(SEQ. ID NO: 1638)
55 5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1630)(SEQ. ID NO: 1639)
5'-GB GTT TCB TCT TG-3' (FRAG. NO:1631)(SEQ. ID NO: 1640)
5'-B GTT TCB TCT TG-3' (FRAG. NO:1632)(SEQ. ID NO: 1641)
5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1633)(SEQ. ID NO: 1642)
5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1634)(SEQ. ID NO: 1643)
60 5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1635)(SEQ. ID NO: 1644)
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1636)(SEQ. ID NO: 1645)
5'-GGB GTT TCB TCT T-3' (FRAG. NO:1637)(SEQ. ID NO: 1646)

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- 5'-GB GTT TCB TCT T-3' (FRAG. NO:1638)(SEQ. ID NO: 1647)
5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1639)(SEQ. ID NO: 1648)
5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1640)(SEQ. ID NO: 1649)
5'-G GGB GTT TCB TCT-3' (FRAG. NO:1641)(SEQ. ID NO: 1650)
5 5'-GGB GTT TCB TCT-3' (FRAG. NO:1642)(SEQ. ID NO: 1651)
5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1643)(SEQ. ID NO: 1652)
5'-GG GGB GTT TCB TC-3' (FRAG. NO:1644)(SEQ. ID NO: 1653)
5'-G GGB GTT TCB TC-3' (FRAG. NO:1645)(SEQ. ID NO: 1654)
5'-GGG GGB GTT TCB T-3' (FRAG. NO:1646)(SEQ. ID NO: 1655)
10 5'-GG GGB GTT TCB T-3' (FRAG. NO:1647)(SEQ. ID NO: 1656)
5'-GGG GGB GTT TCB-3' (FRAG. NO:1648)(SEQ. ID NO: 1657)
5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1649)(SEQ. ID NO: 1658)
5'-TCT CCT GTT CTG GTG TCT CCT C-3' (FRAG. NO:1650)(SEQ. ID NO: 1659)
5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1651)(SEQ. ID NO: 1660)
15 5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1652)(SEQ. ID NO: 1661)
5'-GTT TCG CTC TTG TTG CCC-3' -3' (FRAG. NO:1653)(SEQ. ID NO: 1661)
5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1654)(SEQ. ID NO: 1663)
5'-GGG GGB G-3' (FRAG. NO:1912)(SEQ. ID NO:1925)
5'-GTG GGT GTC C-3' (FRAG. NO:1913) (SEQ. ID NO: 1926)

20 **BP-1 Nucleic Acids and Antisense Oligonucleotide Fragments**

- 5'-CCGTGTTGTC BGTGGTGCTG CCCGTTTGBG GTBTGGCGCT CCBCCBBTTC CCTTTTCTCC TTGTTTCCG
TTTCTCTTGC CGTCTGTGGT T-3' (FRAG. NO:1914) (SEQ. ID NO: 1927)
5'-CCCGTTTGBGGTBTGGC-3'(FRAG. NO:1915) (SEQ. ID NO: 1928)
5'-GCTCCBCCBBTTCCTTTTCTCC-3'(FRAG. NO:1916) (SEQ. ID NO: 1929)
25 5'-TTGTTTTCGTTTCTCTTG-3'(FRAG. NO:1917) (SEQ. ID NO: 1930)
5'-CCGTCTGTGGT-3'(FRAG. NO:1918) (SEQ. ID NO: 1931)
5'-CCCGTTTGAGGTATGGC-3'(FRAG. NO:1919) (SEQ. ID NO: 1932)
5'-GCTCCBCCAATTCCTTTTCTCC-3'(FRAG. NO:1920) (SEQ. ID NO: 1933)

C/EBPNucleic Acids and Antisense Oligonucleotide Antisense Oligonucleotide Fragments

- 30 5'-GGGCCCCGCCCCGCCCTTTTCTBGCCCC GGCC-3' (FRAG. NO:1921) (SEQ. ID NO: 1934)
5'-GGGCCCCGCCCCGCCCTTTTCTBGCCCC GGC-3' (FRAG. NO:1922) (SEQ. ID NO: 1935)
5'-GGGCCCC GCCCCGCCCTTTTCTBGCCCCGG-3' (FRAG. NO:1923) (SEQ. ID NO: 1936)
5'-GGGCCCCGCCCCGCCCTTTTCTBGCCCCG-3' (FRAG. NO:1924) (SEQ. ID NO: 1937)
5'-GGGCCCCGCCCCGCCCTTTTCTBGCCCC-3' (FRAG. NO:1925) (SEQ. ID NO: 1938)
35 5'-GGGCCCCGCCCCGCCCTTTTCTBGCCCC-3' (FRAG. NO:1926) (SEQ. ID NO: 1939)
5'-GGGCCCCGCCCCGCCCTTTTCTBGCC-3' (FRAG. NO:1927) (SEQ. ID NO: 1940)
5'-GGGCCCCGCCCCGCCCTTTTCTBGC-3' (FRAG. NO:1928) (SEQ. ID NO: 1941)
5'-GGGCCCCGCCCCGCCCTTTTCTBG-3' (FRAG. NO:1929) (SEQ. ID NO: 1942)
5'-GGGCCCCGCCCCGCCCTTTTCTB-3' (FRAG. NO:1930) (SEQ. ID NO: 1943)
40 5'-GGGCCCCGCCCCGCCCTTTTCT-3' (FRAG. NO:1931) (SEQ. ID NO:1942) 1944)
5'-GGGCCCCGCCCCGCCCTTTTC-3' (FRAG. NO:1932) (SEQ. ID NO: 1945)
5'-GGGCCCCGCCCCGCCCTTTT-3' (FRAG. NO:1933) (SEQ. ID NO: 1946)
5'-GGGCCCCGCCCCGCCCTTT-3' (FRAG. NO:1934) (SEQ. ID NO: 1947) [1945]
5'-GGGCCCCGCCCCGCCCTT-3' (FRAG. NO:1935) (SEQ. ID NO: 1948)
45 5'-GGGCCCCGCCCCGCCCT-3' (FRAG. NO:1936) (SEQ. ID NO: 1949)
5'-GGGCCCCGCCCCGCC-3' (FRAG. NO:1937) (SEQ. ID NO: 1950)
5'-GGGCCCCGCCCCGCC-3' (FRAG. NO:1938) (SEQ. ID NO: 1951)
5'-GGGCCCCGCCCCGCC-3' (FRAG. NO:1939) (SEQ. ID NO: 1952)
5'-GGGCCCCGCCCCGCC-3' (FRAG. NO:1940) (SEQ. ID NO: 1953)
50 5'-GGGCCCCGCCCCGC-3' (FRAG. NO:1941) (SEQ. ID NO: 1954)
5'-GGGCCCCGCCCCG-3' (FRAG. NO:1942) (SEQ. ID NO: 1955)
5'-GGGCCCCGCCCC-3' (FRAG. NO:1943) (SEQ. ID NO: 1956)
5'-GGGCCCCGCCCC-3' (FRAG. NO:1944) (SEQ. ID NO: 1957)
5'-GGCCCCGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1945) (SEQ. ID NO: 1958)
55 5'-GCCBGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1946) (SEQ. ID NO: 1959)
5'-CCCBGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1947) (SEQ. ID NO: 1960)
5'-CCBGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO: 1961)
5'-CBGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO: 1962)
5'-BGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1950) (SEQ. ID NO: 1963)
60 5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1951) (SEQ. ID NO: 1964)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1952) (SEQ. ID NO: 1965)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1953) (SEQ. ID NO: 1966)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1954) (SEQ. ID NO: 1967)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1955) (SEQ. ID NO: 1968)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1956) (SEQ. ID NO: 1969)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1957) (SEQ. ID NO: 1970)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1958) (SEQ. ID NO: 1971)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1959) (SEQ. ID NO: 1972)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1960) (SEQ. ID NO: 1973)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1961) (SEQ. ID NO: 1974)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1962) (SEQ. ID NO: 1975)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1963) (SEQ. ID NO: 1976)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1964) (SEQ. ID NO: 1977)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1965) (SEQ. ID NO: 1978)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1966) (SEQ. ID NO: 1979)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1967) (SEQ. ID NO: 1980)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1968) (SEQ. ID NO: 1981)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1969) (SEQ. ID NO: 1982)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1970) (SEQ. ID NO: 1983)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1971) (SEQ. ID NO: 1984)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1972) (SEQ. ID NO: 1985)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1973) (SEQ. ID NO: 1986)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1974) (SEQ. ID NO: 1987)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1975) (SEQ. ID NO: 1988)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1976) (SEQ. ID NO: 1989)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1977) (SEQ. ID NO: 1990)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1978) (SEQ. ID NO: 1991)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1979) (SEQ. ID NO: 1992)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1980) (SEQ. ID NO: 1993)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1981) (SEQ. ID NO: 1994)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1982) (SEQ. ID NO: 1995)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1983) (SEQ. ID NO: 1996)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1984) (SEQ. ID NO: 1997)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1985) (SEQ. ID NO: 1998)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1986) (SEQ. ID NO: 1999)
5'-GGCCCCGCCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1987) (SEQ. ID NO: 2000)

- 5'-CCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1952) (SEQ. ID NO: 1965)
5'-CCCCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1953) (SEQ. ID NO: 1966)
5'-CCGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1954) (SEQ. ID NO: 1967)
5'-CGCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1955) (SEQ. ID NO: 1968)
15 5'-GCCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1956) (SEQ. ID NO: 1969)
5'-CCGCTTTTCTBGCCCCGGC-3' (FRAG. NO:1957) (SEQ. ID NO: 1970)
5'-CGCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1958) (SEQ. ID NO: 1971)
5'-GCCTTTTCTBGCCCCGGC-3' (FRAG. NO:1959) (SEQ. ID NO: 1972)
5'-CCTTTTCTBGCCCCGGC-3' (FRAG. NO:1960) (SEQ. ID NO: 1973)
10 5'-CTTTTCTBGCCCCGGC-3' (FRAG. NO:1961) (SEQ. ID NO: 1974)
5'-TTTTCTBGCCCCGGC-3' (FRAG. NO:1962) (SEQ. ID NO: 1975)
5'-TTTCTBGCCCCGGC-3' (FRAG. NO:1963) (SEQ. ID NO: 1976)
5'-TTCTBGCCCCGGC-3' (FRAG. NO:1964) (SEQ. ID NO: 1977)
5'-TCTBGCCCCGGC-3' (FRAG. NO:1965) (SEQ. ID NO: 1978)
15 5'-CTBGCCCCGGC-3' (FRAG. NO:1966) (SEQ. ID NO: 1979)
5'-GCGBGGCTGTBCCTCGCTGGGCCC-3' (FRAG. NO:1967) (SEQ. ID NO: 1980)
5'-GCGBGGCTGTBCCTCGCTGGGCC-3' (FRAG. NO:1968) (SEQ. ID NO: 1981)
5'-GCGBGGCTGTBCCTCGCTGGGC-3' (FRAG. NO:1969) (SEQ. ID NO: 1982)
5'-GCGBGGCTGTBCCTCGCTGGG-3' (FRAG. NO:1970) (SEQ. ID NO:1983)
20 5'-GCGBGGCTGTBCCTCGCTGG-3' (FRAG. NO:1971) (SEQ. ID NO:1984)
5'-GCGBGGCTGTBCCTCGCTG-3' (FRAG. NO:1972) (SEQ. ID NO:1985)
5'-GCGBGGCTGTBCCTCGCT-3' (FRAG. NO:1973) (SEQ. ID NO:1986)
5'-GCGBGGCTGTBCCTCGC-3' (FRAG. NO:1974) (SEQ. ID NO:1987)
5'-GCGBGGCTGTBCCTCG-3' (FRAG. NO:1975) (SEQ. ID NO:1988)
25 5'-GCGBGGCTGTBCCTC-3' (FRAG. NO:1976) (SEQ. ID NO:1989)
5'-GCGBGGCTGTBCCT-3' (FRAG. NO:1977) (SEQ. ID NO:1990)
5'-GCGBGGCTGTBCC-3' (FRAG. NO:1978) (SEQ. ID NO:1991)
5'-GCGBGGCTGTBC-3' (FRAG. NO:1979) (SEQ. ID NO:1992)
5'-GCGBGGCTGTB-3' (FRAG. NO:1980) (SEQ. ID NO:1993)
30 5'-GCGBGGCTGT-3' (FRAG. NO:1981) (SEQ. ID NO:1994)
5'-GCGBGGCTG-3' (FRAG. NO:1982) (SEQ. ID NO:1995)
5'-CGBGGCTGTBCCTCGCTGGGCCC-3' (FRAG. NO:1983) (SEQ. ID NO:1996)
5'-GBGGCTGTBCCTCGCTGGGCCC-3' (FRAG. NO:1984) (SEQ. ID NO:1997)
5'-BGGCTGTBCCTCGCTGGGCCC-3' (FRAG. NO:1985) (SEQ. ID NO:1998)
35 5'-GGCTGTBCCTCGCTGGGCCC-3' (FRAG. NO:1986) (SEQ. ID NO:1999)
5'-GCTGTBCCTCGCTGGGCCC-3' (FRAG. NO:1987) (SEQ. ID NO:2000)
5'-CTGTBCCTCGCTGGGCCC-3' (FRAG. NO:1988) (SEQ. ID NO:2001)
5'-TGTCBCTCGCTGGGCCC-3' (FRAG. NO:1989) (SEQ. ID NO:2002)
5'-GTCBCTCGCTGGGCCC-3' (FRAG. NO:1990) (SEQ. ID NO:2003)
40 5'-TCBCTCGCTGGGCCC-3' (FRAG. NO:1991) (SEQ. ID NO:2004)
5'-CBCCTCGCTGGGCCC-3' (FRAG. NO:1992) (SEQ. ID NO:2005)
5'-BCCTCGCTGGGCCC-3' (FRAG. NO:1993) (SEQ. ID NO:2006)
5'-CCTCGCTGGGCCC-3' (FRAG. NO:1994) (SEQ. ID NO:2007)
5'-CTCGCTGGGCCC-3' (FRAG. NO:1995) (SEQ. ID NO:2008)
45 5'-TCGCTGGGCCC-3' (FRAG. NO:1996) (SEQ. ID NO:2009)
5'-CGCTGGGCCC-3' (FRAG. NO:1997) (SEQ. ID NO:2010)
5'-GCGCGCCGTCBTGGCGGCGTCGGGCCGGG-3' (FRAG. NO:1998) (SEQ. ID NO:2011)
5'-GCGCGCCGTCBTGGCGGCGTCGGGCCGGG-3' (FRAG. NO:1999) (SEQ. ID NO:2012)
5'-GCGCGCCGTCBTGGCGGCGTCGGGCCGG-3' (FRAG. NO:2000) (SEQ. ID NO:2013)
50 5'-GCGCGCCGTCBTGGCGGCGTCGGGCCG-3' (FRAG. NO:2001) (SEQ. ID NO:2014)
5'-GCGCGCCGTCBTGGCGGCGTCGGGCC-3' (FRAG. NO:2002) (SEQ. ID NO:2015)
5'-GCGCGCCGTCBTGGCGGCGTCGGGC-3' (FRAG. NO:2003) (SEQ. ID NO:2016)
5'-GCGCGCCGTCBTGGCGGCGTCGGG-3' (FRAG. NO:2004) (SEQ. ID NO:2017)
5'-GCGCGCCGTCBTGGCGGCGTCGG-3' (FRAG. NO:2005) (SEQ. ID NO:2018)
55 5'-GCGCGCCGTCBTGGCGGCGTCG-3' (FRAG. NO:2006) (SEQ. ID NO:2019)
5'-GCGCGCCGTCBTGGCGGCGTC-3' (FRAG. NO:2007) (SEQ. ID NO:2020)
5'-GCGCGCCGTCBTGGCGGCGT-3' (FRAG. NO:2008) (SEQ. ID NO:2021)
5'-GCGCGCCGTCBTGGCGGC-3' (FRAG. NO:2009) (SEQ. ID NO:2022)
5'-GCGCGCCGTCBTGGCGG-3' (FRAG. NO:2010) (SEQ. ID NO:2023)
60 5'-GCGCGCCGTCBTGGCGG-3' (FRAG. NO:2011) (SEQ. ID NO:2024)
5'-GCGCGCCGTCBTGGCG-3' (FRAG. NO:2012) (SEQ. ID NO:2025)
5'-GCGCGCCGTCBTGGC-3' (FRAG. NO:2013) (SEQ. ID NO:2026)

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- 5'-GCGCGGCCGTCBTGG-3' (FRAG. NO:2014) (SEQ. ID NO:2027)
5'-GCGCGGCCGTCBTG-3' (FRAG. NO:2015) (SEQ. ID NO:2028)
5'-GCGCGGCCGTCBT-3' (FRAG. NO:2016) (SEQ. ID NO:2029)
5'-GCGCGGCCGTCB-3' (FRAG. NO:2017) (SEQ. ID NO:2030)
5 5'-GCGCGGCCGTC-3' (FRAG. NO:2018) (SEQ. ID NO:2031)
5'-GCGCGGCCGT-3' (FRAG. NO:2019) (SEQ. ID NO:2032)
5'-CGCGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2020) (SEQ. ID NO:2033)
5'-GCGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2021) (SEQ. ID NO:2034)
5'-CGGCCGTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2022) (SEQ. ID NO:2035)
10 5'-GGCCGTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2023) (SEQ. ID NO:2036)
5'-GCCGTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2024) (SEQ. ID NO:2037)
5'-CCGTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2025) (SEQ. ID NO:2038)
5'-CGTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2026) (SEQ. ID NO:2039)
5'-GTCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2027) (SEQ. ID NO:2040)
15 5'-TCBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2028) (SEQ. ID NO:2041)
5'-CBTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2029) (SEQ. ID NO:2042)
5'-BTGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2030) (SEQ. ID NO:2043)
5'-TGGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2031) (SEQ. ID NO:2044)
5'-GGCGGCGTCGGGCCGGGC-3' (FRAG. NO:2032) (SEQ. ID NO:2045)
20 5'-GCGGCGTCGGGCCGGGC-3' (FRAG. NO:2033) (SEQ. ID NO:2046)
5'-CGGCGTCGGGCCGGGC-3' (FRAG. NO:2034) (SEQ. ID NO:2047)
5'-GGCGTCGGGCCGGGC-3' (FRAG. NO:2035) (SEQ. ID NO:2048)
5'-GCGTCGGGCCGGGC-3' (FRAG. NO:2036) (SEQ. ID NO:2049)
5'-CGTCGGGCCGGGC-3' (FRAG. NO:2037) (SEQ. ID NO:2050)
25 5'-GTCGGGCCGGGC-3' (FRAG. NO:2038) (SEQ. ID NO:2051)
5'-TCGGGCCGGGC-3' (FRAG. NO:2039) (SEQ. ID NO:2052)
5'-CGGGCCGGGC-3' (FRAG. NO:2040) (SEQ. ID NO:2053)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2041) (SEQ. ID NO:2054)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGGCC-3' (FRAG. NO:2042) (SEQ. ID NO:2055)
30 5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGGC-3' (FRAG. NO:2043) (SEQ. ID NO:2056)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGGG-3' (FRAG. NO:2044) (SEQ. ID NO:2057)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCGG-3' (FRAG. NO:2045) (SEQ. ID NO:2058)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCCG-3' (FRAG. NO:2046) (SEQ. ID NO:2059)
5'-CCGCBGGCCBGGGCGCGCCGCCGGCC-3' (FRAG. NO:2047) (SEQ. ID NO:2060)
35 5'-CCGCBGGCCBGGGCGCGCCGCCGGC-3' (FRAG. NO:2048) (SEQ. ID NO:2061)
5'-CCGCBGGCCBGGGCGCGCCGCCGG-3' (FRAG. NO:2049) (SEQ. ID NO:2062)
5'-CCGCBGGCCBGGGCGCGCCGCCG-3' (FRAG. NO:2050) (SEQ. ID NO:2063)
5'-CCGCBGGCCBGGGCGCGCCGCC-3' (FRAG. NO:2051) (SEQ. ID NO:2064)
5'-CCGCBGGCCBGGGCGCGCCGC-3' (FRAG. NO:2052) (SEQ. ID NO:2065)
40 5'-CCGCBGGCCBGGGCGCGCCG-3' (FRAG. NO:2053) (SEQ. ID NO:2066)
5'-CCGCBGGCCBGGGCGCGCC-3' (FRAG. NO:2054) (SEQ. ID NO:2067)
5'-CCGCBGGCCBGGGCGCGC-3' (FRAG. NO:2055) (SEQ. ID NO:2068)
5'-CCGCBGGCCBGGGCGCG-3' (FRAG. NO:2056) (SEQ. ID NO:2069)
5'-CCGCBGGCCBGGGCGC-3' (FRAG. NO:2057) (SEQ. ID NO:2070)
45 5'-CCGCBGGCCBGGGCG-3' (FRAG. NO:2058) (SEQ. ID NO:2071)
5'-CCGCBGGCCBGGG-3' (FRAG. NO:2059) (SEQ. ID NO:2072)
5'-CCGCBGGCCBGG-3' (FRAG. NO:2060) (SEQ. ID NO:2073)
5'-CCGCBGGCCBG-3' (FRAG. NO:2061) (SEQ. ID NO:2074)
5'-CCGCBGGCCB-3' (FRAG. NO:2062) (SEQ. ID NO:2075)
50 5'-CCGCBGGCCB-3' (FRAG. NO:2063) (SEQ. ID NO:2076)
5'-CCGCBGGCC-3' (FRAG. NO:2064) (SEQ. ID NO:2077)
5'-GCBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2065) (SEQ. ID NO:2078)
5'-GCBGGCCBGGGCGCGCCGCCGGCCGGGCC-3' (FRAG. NO:2066) (SEQ. ID NO:2079)
5'-CBGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2067) (SEQ. ID NO:2080)
55 5'-BGGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2068) (SEQ. ID NO:2081)
5'-GGCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2069) (SEQ. ID NO:2082)
5'-GCCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2070) (SEQ. ID NO:2083)
5'-CCBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2071) (SEQ. ID NO:2084)
5'-CBGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2072) (SEQ. ID NO:2085)
60 5'-BGGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2073) (SEQ. ID NO:2086)
5'-GGGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2074) (SEQ. ID NO:2087)
5'-GGCGCGCCGCCGGCCGGGCCG-3' (FRAG. NO:2075) (SEQ. ID NO:2088)

- 5'-GCGCGCCCGCCGGCCGGGCCG-3' (FRAG. NO:2076) (SEQ. ID NO:2089)
5'-CGCGCCCGCCGGCCGGGCCG-3' (FRAG. NO:2077) (SEQ. ID NO:2090)
5'-GCGCCCGCCGGCCGGGCCG-3' (FRAG. NO:2078) (SEQ. ID NO:2091)
5'-CGCCCGCCGGCCGGGCCG-3' (FRAG. NO:2079) (SEQ. ID NO:2092)
5'-GCCCGCCGGCCGGGCCG-3' (FRAG. NO:2080) (SEQ. ID NO:2093)
5'-CCGCCCGCCGGGCCG-3' (FRAG. NO:2081) (SEQ. ID NO:2094)
5'-CGCCCGCCGGGCCG-3' (FRAG. NO:2082) (SEQ. ID NO:2095)
5'-GCCCGCCGGGCCG-3' (FRAG. NO:2083) (SEQ. ID NO:2096)
5'-CCGCCCGCCGGCCG-3' (FRAG. NO:2084) (SEQ. ID NO:2097)
5'-CGGCCCGGCCG-3' (FRAG. NO:2085) (SEQ. ID NO:2098)
5'-GGCCGGGCCG-3' (FRAG. NO:2086) (SEQ. ID NO:2099)
5'-GGGCGCBGGCTCCGCB-3' (FRAG. NO:2087) (SEQ. ID NO:2100)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2088) (SEQ. ID NO:2101)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2089) (SEQ. ID NO:2102)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2090) (SEQ. ID NO:2103)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2091) (SEQ. ID NO:2104)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGC-3' (FRAG. NO:2092) (SEQ. ID NO:2105)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGG-3' (FRAG. NO:2093) (SEQ. ID NO:2106)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCG-3' (FRAG. NO:2094) (SEQ. ID NO:2107)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCG-3' (FRAG. NO:2095) (SEQ. ID NO:2108)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCG-3' (FRAG. NO:2096) (SEQ. ID NO:2109)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGC-3' (FRAG. NO:2097) (SEQ. ID NO:2110)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCG-3' (FRAG. NO:2098) (SEQ. ID NO:2111)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCG-3' (FRAG. NO:2099) (SEQ. ID NO:2112)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCC-3' (FRAG. NO:2100) (SEQ. ID NO:2113)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGC-3' (FRAG. NO:2101) (SEQ. ID NO:2114)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTG-3' (FRAG. NO:2102) (SEQ. ID NO:2115)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTT-3' (FRAG. NO:2103) (SEQ. ID NO:2116)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCT-3' (FRAG. NO:2104) (SEQ. ID NO:2117)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGC-3' (FRAG. NO:2105) (SEQ. ID NO:2118)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGG-3' (FRAG. NO:2106) (SEQ. ID NO:2119)
5'-GGGCCCTGGCTCGGCCCGCGGCCCG-3' (FRAG. NO:2107) (SEQ. ID NO:2120)
5'-GGGCCCTGGCTCGGCCCGCGGCCCG-3' (FRAG. NO:2108) (SEQ. ID NO:2121)
5'-GGGCCCTGGCTCGGCCCGCGGCCCG-3' (FRAG. NO:2109) (SEQ. ID NO:2122)
5'-GGGCCCTGGCTCGGCCCGCGGC-3' (FRAG. NO:2110) (SEQ. ID NO:2123)
5'-GGGCCCTGGCTCGGCCCGCGG-3' (FRAG. NO:2111) (SEQ. ID NO:2124)
5'-GGGCCCTGGCTCGGCCCGCG-3' (FRAG. NO:2112) (SEQ. ID NO:2125)
5'-GGGCCCTGGCTCGGCCCGC-3' (FRAG. NO:2113) (SEQ. ID NO:2126)
5'-GGGCCCTGGCTCGGCCCG-3' (FRAG. NO:2114) (SEQ. ID NO:2127)
5'-GGGCCCTGGCTCGGCCCG-3' (FRAG. NO:2115) (SEQ. ID NO:2128)
5'-GGGCCCTGGCTCGGCCCG-3' (FRAG. NO:2116) (SEQ. ID NO:2129)
5'-GGGCCCTGGCTCGGCC-3' (FRAG. NO:2117) (SEQ. ID NO:2130)
5'-GGGCCCTGGCTCGGC-3' (FRAG. NO:2118) (SEQ. ID NO:2131)
5'-GGGCCCTGGCTCGG-3' (FRAG. NO:2119) (SEQ. ID NO:2132)
5'-GGGCCCTGGCTCG-3' (FRAG. NO:2120) (SEQ. ID NO:2133)
5'-GGGCCCTGGCTC-3' (FRAG. NO:2121) (SEQ. ID NO:2134)
5'-GGGCCCTGGCT-3' (FRAG. NO:2122) (SEQ. ID NO:2135)
5'-GGGCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2123) (SEQ. ID NO:2136)
5'-GCCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2124) (SEQ. ID NO:2137)
5'-CCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2125) (SEQ. ID NO:2138)
5'-CCCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2126) (SEQ. ID NO:2139)
5'-CCTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2127) (SEQ. ID NO:2140)
5'-CTGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2128) (SEQ. ID NO:2141)
5'-TGGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2129) (SEQ. ID NO:2142)
5'-GGCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2130) (SEQ. ID NO:2143)
5'-GCTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2131) (SEQ. ID NO:2144)
5'-CTCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2132) (SEQ. ID NO:2145)
5'-TCGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2133) (SEQ. ID NO:2146)
5'-CGGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2134) (SEQ. ID NO:2147)
5'-GGCCCGCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2135) (SEQ. ID NO:2148)
5'-GCCCCCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2136) (SEQ. ID NO:2149)
5'-CCCCCGGCCCGGCTTGCCCGCCCGGCCCG-3' (FRAG. NO:2137) (SEQ. ID NO:2150)

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5'-CCCGCGGCCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2138) (SEQ. ID NO:2151)
5'-CCGCGGCCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2139) (SEQ. ID NO:2152)
5'-CGCGGCCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2140) (SEQ. ID NO:2153)
5'-GCGGCCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2141) (SEQ. ID NO:2154)
5'-CGGCCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2142) (SEQ. ID NO:2155)
5'-GGCCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2143) (SEQ. ID NO:2156)
5'-GCCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2144) (SEQ. ID NO:2157)
5'-CCCCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2145) (SEQ. ID NO:2158)
5'-CCGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2146) (SEQ. ID NO:2159)
5'-CGGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2147) (SEQ. ID NO:2160)
5'-GGCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2148) (SEQ. ID NO:2161)
5'-GCTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2149) (SEQ. ID NO:2162)
5'-CTTGCCCGCCCGGCCCGG-3' (FRAG. NO:2150) (SEQ. ID NO:2163)
5'-TTGCCCGCCCGGCCCGG-3' (FRAG. NO:2151) (SEQ. ID NO:2164)
5'-TGCCCGCCCGGCCCGG-3' (FRAG. NO:2152) (SEQ. ID NO:2165)
5'-GCCCCCGCCCGGCCCGG-3' (FRAG. NO:2153) (SEQ. ID NO:2166)
5'-CCCCCGCCCGGCCCGG-3' (FRAG. NO:2154) (SEQ. ID NO:2167)
5'-CCGCCCCCGGCCCGG-3' (FRAG. NO:2155) (SEQ. ID NO:2168)
5'-CGCCCCCGGCCCGG-3' (FRAG. NO:2156) (SEQ. ID NO:2169)
5'-GCCCCCGGCCCGG-3' (FRAG. NO:2157) (SEQ. ID NO:2170)
5'-GGCGGGGGCGGCGGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2158) (SEQ. ID NO:2171)
5'-GGCGGGGGCGGCGGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2159) (SEQ. ID NO:2172)
5'-GGCGGGGGCGGCGGCCTGGCTCGCCTBGGGCC-3' (FRAG. NO:2160) (SEQ. ID NO:2173)
5'-GGCGGGGGCGGCGGCCTGGCTCGCCTBGGGC-3' (FRAG. NO:2161) (SEQ. ID NO:2174)
5'-GGCGGGGGCGGCGGCCTGGCTCGCCTBGGG-3' (FRAG. NO:2162) (SEQ. ID NO:2175)
5'-GGCGGGGGCGGCGGCCTGGCTCGCCTBGG-3' (FRAG. NO:2163) (SEQ. ID NO:2176)
5'-GGCGGGGGCGGCGGCCTGGCTCGCCTBG-3' (FRAG. NO:2164) (SEQ. ID NO:2177)
5'-GGCGGGGGCGGCGGCCTGGCTCGCCTB-3' (FRAG. NO:2165) (SEQ. ID NO:2178)
5'-GGCGGGGGCGGCGGCCTGGCTCGCCT-3' (FRAG. NO:2166) (SEQ. ID NO:2179)
5'-GGCGGGGGCGGCGGCCTGGCTCGCC-3' (FRAG. NO:2167) (SEQ. ID NO:2180)
5'-GGCGGGGGCGGCGGCCTGGCTCGC-3' (FRAG. NO:2168) (SEQ. ID NO:2181)
5'-GGCGGGGGCGGCGGCCTGGCTCG-3' (FRAG. NO:2169) (SEQ. ID NO:2182)
5'-GGCGGGGGCGGCGGCCTGGCTC-3' (FRAG. NO:2170) (SEQ. ID NO:2183)
5'-GGCGGGGGCGGCGGCCTGGCT-3' (FRAG. NO:2171) (SEQ. ID NO:2184)
5'-GGCGGGGGCGGCGGCCTGGC-3' (FRAG. NO:2172) (SEQ. ID NO:2185)
5'-GGCGGGGGCGGCGGCCTGG-3' (FRAG. NO:2173) (SEQ. ID NO:2186)
5'-GGCGGGGGCGGCGGCCTG-3' (FRAG. NO:2174) (SEQ. ID NO:2187)
5'-GGCGGGGGCGGCGGCCT-3' (FRAG. NO:2175) (SEQ. ID NO:2188)
5'-GGCGGGGGCGGCGGCC-3' (FRAG. NO:2176) (SEQ. ID NO:2189)
5'-GGCGGGGGCGGCGGCGC-3' (FRAG. NO:2177) (SEQ. ID NO:2190)
5'-GGCGGGGGCGGCGGCG-3' (FRAG. NO:2178) (SEQ. ID NO:2191)
5'-GGCGGGGGCGGCGGC-3' (FRAG. NO:2179) (SEQ. ID NO:2192)
5'-GGCGGGGGCGGCGG-3' (FRAG. NO:2180) (SEQ. ID NO:2193)
5'-GGCGGGGGCGGCG-3' (FRAG. NO:2181) (SEQ. ID NO:2194)
5'-GGCGGGGGCGG-3' (FRAG. NO:2182) (SEQ. ID NO:2195)
5'-GGCGGGGGCGG-3' (FRAG. NO:2183) (SEQ. ID NO:2196)
5'-GCGGGGGCGGCGGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2184) (SEQ. ID NO:2197)
5'-CGGGGGCGGCGGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2185) (SEQ. ID NO:2198)
5'-GGGGCGGCGGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2186) (SEQ. ID NO:2199)
5'-GGGGCGGCGGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2187) (SEQ. ID NO:2200)
5'-GGGCGGCGGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2188) (SEQ. ID NO:2201)
5'-GGCGGCGGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2189) (SEQ. ID NO:2202)
5'-GCGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2190) (SEQ. ID NO:2203)
5'-CGGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2191) (SEQ. ID NO:2204)
5'-GGCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2192) (SEQ. ID NO:2205)
5'-GCGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2193) (SEQ. ID NO:2206)
5'-CGGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2194) (SEQ. ID NO:2207)
5'-GGCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2195) (SEQ. ID NO:2208)
5'-GCGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2196) (SEQ. ID NO:2209)
5'-CGCCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2197) (SEQ. ID NO:2210)
5'-GCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2198) (SEQ. ID NO:2211)
5'-CCTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2199) (SEQ. ID NO:2212)

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- 5'-CTGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2200) (SEQ. ID NO:2213)
5'-TGGCTCGCCTBGGGCCCC-3' (FRAG. NO:2201) (SEQ. ID NO:2214)
5'-GGCTCGCCTBGGGCCCC-3' (FRAG. NO:2202) (SEQ. ID NO:2215)
5'-GCTCGCCTBGGGCCCC-3' (FRAG. NO:2203) (SEQ. ID NO:2216)
5 5'-CTCGCCTBGGGCCCC-3' (FRAG. NO:2204) (SEQ. ID NO:2217)
5'-TCGCCTBGGGCCCC-3' (FRAG. NO:2205) (SEQ. ID NO:2218)
5'-CGCCTBGGGCCCC-3' (FRAG. NO:2206) (SEQ. ID NO:2219)
5'-GCCTBGGGCCCC-3' (FRAG. NO:2207) (SEQ. ID NO:2220)
5'-CCTBGGGCCCC-3' (FRAG. NO:2208) (SEQ. ID NO:2221)
10 5'-CTBGGGCCCC-3' (FRAG. NO:2209) (SEQ. ID NO:2222)
5'-GGGTGGGCBGCGCGGCC-3' (FRAG. NO:2210) (SEQ. ID NO:2223)
5'-GGTCGGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2211) (SEQ. ID NO:2224)
5'-GGTCGGCGBBBGCTCGTCGTGG-3' (FRAG. NO:2212) (SEQ. ID NO:2225)
5'-GGTCGGCGBBBGCTCGTCGTG-3' (FRAG. NO:2213) (SEQ. ID NO:2226)
15 5'-GGTCGGCGBBBGCTCGTCGT-3' (FRAG. NO:2214) (SEQ. ID NO:2227)
5'-GGTCGGCGBBBGCTCGTCG-3' (FRAG. NO:2215) (SEQ. ID NO:2228)
5'-GGTCGGCGBBBGCTCGTC-3' (FRAG. NO:2216) (SEQ. ID NO:2229)
5'-GGTCGGCGBBBGCTCGT-3' (FRAG. NO:2217) (SEQ. ID NO:2230)
5'-GGTCGGCGBBBGCTCG-3' (FRAG. NO:2218) (SEQ. ID NO:2231)
20 5'-GGTCGGCGBBBGCTC-3' (FRAG. NO:2219) (SEQ. ID NO:2232)
5'-GGTCGGCGBBBGCT-3' (FRAG. NO:2220) (SEQ. ID NO:2233)
5'-GGTCGGCGBBBG-3' (FRAG. NO:2221) (SEQ. ID NO:2234)
5'-GGTCGGCGBBBG-3' (FRAG. NO:2222) (SEQ. ID NO:2235)
5'-GGTCGGCGBBB-3' (FRAG. NO:2223) (SEQ. ID NO:2236)
25 5'-GGTCGGCGBB-3' (FRAG. NO:2224) (SEQ. ID NO:2237)
5'-GTCGGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2225) (SEQ. ID NO:2238)
5'-TCGGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2226) (SEQ. ID NO:2239)
5'-CGGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2227) (SEQ. ID NO:2240)
5'-GGCGBBBGCTCGTCGTGGC-3' (FRAG. NO:2228) (SEQ. ID NO:2241)
30 5'-GCCBBBGCTCGTCGTGGC-3' (FRAG. NO:2229) (SEQ. ID NO:2242)
5'-CGBBBGCTCGTCGTGGC-3' (FRAG. NO:2230) (SEQ. ID NO:2243)
5'-BBBBGCTCGTCGTGGC-3' (FRAG. NO:2231) (SEQ. ID NO:2244)
5'-BBBGCTCGTCGTGGC-3' (FRAG. NO:2232) (SEQ. ID NO:2245)
5'-BGBGCTCGTCGTGGC-3' (FRAG. NO:2233) (SEQ. ID NO:2246)
35 5'-GBGCTCGTCGTGGC-3' (FRAG. NO:2234) (SEQ. ID NO:2247)
5'-BGCTCGTCGTGGC-3' (FRAG. NO:2235) (SEQ. ID NO:2248)
5'-GCTCGTCGTGGC-3' (FRAG. NO:2236) (SEQ. ID NO:2249)
5'-CTCGTCGTGGC-3' (FRAG. NO:2237) (SEQ. ID NO:2250)
5'-TCCTCGTCGTGGC-3' (FRAG. NO:2238) (SEQ. ID NO:2251)
40 5'-GGGGCCCCGCGCCGCCGCC-3' (FRAG. NO:2239) (SEQ. ID NO:2252)
5'-GGGGCCCCGCGCCGCCGC-3' (FRAG. NO:2240) (SEQ. ID NO:2253)
5'-GGGGCCCCGCGCCGCCG-3' (FRAG. NO:2241) (SEQ. ID NO:2254)
5'-GGGGCCCCGCGCCGCC-3' (FRAG. NO:2242) (SEQ. ID NO:2255)
5'-GGGGCCCCGCGCCGC-3' (FRAG. NO:2243) (SEQ. ID NO:2256)
45 5'-GGGGCCCCGCGCCG-3' (FRAG. NO:2244) (SEQ. ID NO:2257)
5'-GGGGCCCCGCGCC-3' (FRAG. NO:2245) (SEQ. ID NO:2258)
5'-GGGGCCCCGCGC-3' (FRAG. NO:2246) (SEQ. ID NO:2259)
5'-GGGGCCCCGCG-3' (FRAG. NO:2247) (SEQ. ID NO:2260)
5'-GGGGCCCCGCGCCGCCGCC-3' (FRAG. NO:2248) (SEQ. ID NO:2261)
50 5'-GGCCCCGCGCCGCCGCC-3' (FRAG. NO:2249) (SEQ. ID NO:2262)
5'-GCCCCGCGCCGCCGCC-3' (FRAG. NO:2250) (SEQ. ID NO:2263)
5'-CCCCGCGCCGCCGCC-3' (FRAG. NO:2251) (SEQ. ID NO:2264)
5'-CCCGCGCCGCCGCC-3' (FRAG. NO:2252) (SEQ. ID NO:2265)
5'-CCGCGCCGCCGCC-3' (FRAG. NO:2253) (SEQ. ID NO:2266)
55 5'-CGCGCCGCCGCC-3' (FRAG. NO:2254) (SEQ. ID NO:2267)
5'-GCGCCGCCGCC-3' (FRAG. NO:2255) (SEQ. ID NO:2268)
5'-CGCCGCCGCC-3' (FRAG. NO:2256) (SEQ. ID NO:2269)
5'-GCCGCCGCC-3' (FRAG. NO:2257) (SEQ. ID NO:2270)
5'-GGGGCGCGGGGGCGCCGGG-3' (FRAG. NO:2258) (SEQ. ID NO:2271)
60 5'-GGCGGGGCBGCGGGCCGGGCC-3' (FRAG. NO:2259) (SEQ. ID NO:2272)
5'-GGCGCGCTCGCGTCGCCCCBGTCGGGCTCGCGC-3' (FRAG. NO:2260) (SEQ. ID NO:2273)
5'-GCGCGGGCBBCBGCGBGCCGGGCGCG-3' (FRAG. NO:2261) (SEQ. ID NO:2274)

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- 5'-GCGCBCGGGGCCBCCTGCGCGGGC-3' (FRAG. NO:2262) (SEQ. ID NO:2275)
 5'-GGGCGGGGTGGGCTGCCCTGCGGCCGCC-3' (FRAG. NO:2263) (SEQ. ID NO:2276)
 5'-GGGCTGCTGCGCGGCGGCTCCGGCGA-3' (FRAG. NO:2264) (SEQ. ID NO:2277)
 5'-CTCCCGGGCGGGGCGGGCGCGGG-3' (FRAG. NO:2265) (SEQ. ID NO:2278)
 5'-GGGCTGCCGCGGTCCGGGCCCTCTTGCCGGCG-3' (FRAG. NO:2266) (SEQ. ID NO:2279)
 5'-GCGCTCGCGCCGCTGCCGG-3' (FRAG. NO:2267) (SEQ. ID NO:2280)
 5'-GCGCCGCTTGCCCTTGTCGCGGC-3' (FRAG. NO:2268) (SEQ. ID NO:2281)
 5'-GCTGCTCCBCGCTGG-3' (FRAG. NO:2269) (SEQ. ID NO:2282)
 5'-GCCGGBGGCCGGCCBGGTCCCGCG-3' (FRAG. NO:2270) (SEQ. ID NO:2283)
 5'-CCCGCGGCCGGCBGGBGGGCGGGCTGGGC-3' (FRAG. NO:2271) (SEQ. ID NO:2284)
 5'-GTCTCTCCCGCCCCGGCCGCGC-3' (FRAG. NO:2272) (SEQ. ID NO:2285)
 5'-GGGCGTCCGCTCCGGGCCGTCGGG-3' (FRAG. NO:2273) (SEQ. ID NO:2286)
 5'-GCGGGCACGCGCGGCTCTGGCGTCGGC-3' (FRAG. NO:2274) (SEQ. ID NO:2287)

Bradykinin Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

- 15 5'-GGTGBCBTTG BGCBTGTCGG CGCGGTCCCG TTBBGBGTGG GCCCGCCAGC CCAGCCACTC CACTTGGGGG
 CGGGTGGCCA GCACGAACAG CACCCAGAGG AAGGGGGGCG GCCCAGAAGG GCAGCCCGCA GGCCAGGATC
 AGGTCTGCTG CGGCCGGAGA TAATGGCATT CACCACGCGG CGGCCAGCG CACGCCGCGC ATCCGGCCCCG
 GGTCTGACC TGCAGCCCC GTCTCCTTGG CATTCTGGG CCCAGTCAC TCCTCTCCCT GCCCCCTTG
 CTGGGGCAGG GACGGGGTG BCBTTGBGCB TGTCGGCGCG GTCCCGTTBB GBGTGGGCCC GCCAGCCCAG
 20 CCACTCCA CTGGGGGCGGG TGGCCAGCAC GAACAGCACC CAGAGGAAGG GGGGCGGCC AGAAGGGCAG
 CCCGAGGCC AGGATCAGGT CTGCTGCGGC CGGAGATAAT GGCATTACAC ACGCGGCGGC CCAGCGCACG
 CCGCGCATCC GGCCCGGGT CTGACCTGCA GCCCCGTCT CTTGGCATT CCTGGGCCCC AGTCACTCCT
 CTCCTGCC CCCTTGCTGG GGCAGGGACG GCCGTGTTGT CBGTGGTGCT GCCCGTTTGB GGTBTGGCGC
 TCCBCCBTT CCCTTTCTC CTGTTTTCC GTTCTCTTG CCGTCTGTGG TT CAGATTCACA AACTGCAGGA
 25 CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGAAGGA TTGAGGGACA
 GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTTGATG
 TCTCCGTAA AACACCGGAG ACTAATTCCT GCCCTGCCA ATTTGACAG GAGCATGGCT GTGAGGATGG
 GGTGAACCA CGCACAGCA AGGACTCAA AATCACAACA GCATTACTGT TCTATTTCG TGCCACACCT
 GAGCCAGCCT GTCCTTCCC AGGAGTGGAG GAGGCTGGG GGGAGGGAGA GGAGTGACTG AGCTTCCCTC
 30 CCGTGTGTT TCCGTCCCTG CCCAGCAAG ACAACTTAGA TCTCCAGGAG AACTGCCATC CAGCTTTGGT
 GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT CTTAATCTA TTCAGCTAGA ACTTTGAAGG
 ACAATTTCT GCATTAATA AGGTAAAGCC CTGAGGGGTC CCTGATAACA ACCTGGAGAC CAGGATTTTA
 TGGCTCCCCT CACTGATGGA CAAGGAGGTC TGTGCCAAAG AAGAATCCAA TAAGCACATA TTGAGCACTT
 GCTGTATATG CAGTATTGAG CACTGTAGGC AAGACCCAAG AAAGAGAAGG AGCCATCTCC ATCTGAAGG
 35 AACTCAAAGA CTCAAGTGGG AACGACTGGG CACTGCCACC ACCAGAAAGC TGTTGACGA GACGTCGAG
 CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGAGAC CAAGGTCCA GCTCAACCAA TAACTATTGC
 ACAACCACCT GTCCTGCCT CAGTTCCCTT TTATGTAACA TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA
 CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC ATGTGAGGCA TCATTACGCA GACGTAACCTG
 GGATATGTT ACTATAAGGA AAAGACACTG AGGTCTAGAA ATAGCTCCGT GGAGCAGAAT CAGTATTGGG
 40 AGCCGGTGGC GGTGTGAAGC ACCAGTGTCT GGCACACAGT AGGTGCTCAT TGGTCCCTT CCACCTGTCA
 TTCCACCAC CTGAGGCC CAACCGCCAC ACACACAGGA GCATTGGAG AGAAGGCCAT GTCTCAAAG
 TCTGATTTGT GATGAGGCAG AGGAAGATAT TTCTAATCGG TCTTGCCAG AGGATCACAG TGCTGAGACC
 CCCACCACC AGCCGTACC TGGGAAGGG GAGAGTGCAG GCCTGCTCAG GGACTGTTCC TGTCTCAGCA
 ACCAAGGGAT TGTCTGTC AATCAATGGT TTATTGGAAG GTGGCCAGT ATGAGCCCTA GAAGAGTGTG
 45 AAAAGGAATG GCAATGGTGT TCACCATCGG CAGTGCCAGG GCAGCACTCA TTTACTTGAT AAATGAATAT
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 CTAGAAGCTG GAGGACTAGA ACCTGGAGGG CTGGAATCTG AAGGGCTAGA ACCTGGAGGG CTGGAATCTG
 GAGAGCTAGA ACCTGGAGGG CTAGAACCTG GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTGG
 50 AATCTGGAGA GCTAGAACCT GGAGGGCTAG AACCTGGAGG GCTAGAACCT AGAAGGGCTA GAACCTGGAG
 GGCTAGAAC TGGCAGGTTA GAACCTAGAA GGGCTAGAAC CTGGAGAGCC AGAACCTGGA GGGCTAGAAC
 CTGGAAGGGC TAGAACCTGT AGAGCTAGAA CATGGAGAGC TAGAACCCGG CAGGCTAGAA CCTGGCAAGC
 TAGAACCTGG AGGGAATGAA CCTGGAGGGC TAGAACCTGG AGAATGAGAA AAATTTACAT GGCAAAGAGC
 CCATAATCC TGACCAATCC AACTCTGAAT TTTAAAGCAA AAGCGTGAAA AAAAAGATT CCTCTTACC
 55 GCGAAG CTTGCTGCG CAGCAAGGAG TTTGCTGCG CTGAGTAACT ATCTGACCA AGAAAAAGC

5 CCGTCAATAA TTTGTAAAT GCTTTTAAAT ATGAATGCTT TAAGCCGGGT GCAGTGCCTC ACATCTGTAA
 TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT GGCCAACATG
 GCAAAACCTC ACTCTCTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG TGATCCCAGC
 TACTCAGGAG GCTGAGACAG GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC AAGATTACGC
 10 CATTTGACTC CAGCCTGGGT GACAGAGAGA GACTCCGTCT CAAAAAATAA AAAAAAATAA AAAAAATTAC
 GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT TCTATGAGCC CAGGAGGGCC TCTCAGAGAG
 GAAAGCTCCT AGGTCTTCCT TTCCTCTGCT AAATCCCTG CTTGAAGGT TCAGAAGGAC TGTGCGTGCT
 CGTTGCATCC TTTGCAAGTG TCCAAACCTT GATCCCAGCT GTGCTTAGGG GTTCCTGCAA ACCTTTTCCA
 GGTGTAAATT ACCTCCCACT TCATTTCTCT TTTACCAACT CAGCTTTTGT TTTAGTGTG TTTGAATTCC
 15 CTGAACTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG AAACCCAGGT
 GCCGGGTGTT GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC ACACACACAC
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 50 CCTCGCCATC TGTATCCTCC AATCACTTCA GTGCTTTGCT GCATAGAAGG TAACGGAAAT CACGATGCCA
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 AAGTTGACCA ATCCCTTGG GAGGGCCCCG GTTGATAAGG AAGGAACGTG AATCCTCCCA TCACGGAAGC
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 55 CCAGTGAGAG CTCGAGATGA AGAACATGAG GCCCCGTTT AGAACCAAGG ATCAGAGGGG GCTCTGTAAG
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 60 CCCCCTTCCT CTGGGTGCTG TTCGTGCTGG CCACCCTAGA GAACATCTTT GTCCTCAGCG TCTTCTGCCT
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 TGCGGGCTGC CCTTCTGGGC CATCACCATC TCCAACAAC TCGACTGGCT CTTTGGGGAG ACGCTCTGCC

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Parameter	Unit	Value
Temperature	°C	25.0
Pressure	atm	1.0
Flow rate	L/min	1.0
Sample concentration	mg/mL	0.1
Mobile phase		H ₂ O/MeOH (90/10)
Detection wavelength	nm	254
Injection volume	μL	10
Column		Agilent Zorbax SB-C18
Column dimensions	mm	150 × 4.6
Particle size	μm	5
Porosity	Å	100
Flow rate	mL/min	1.0
Temperature	°C	30
Pressure	MPa	10
Sample concentration	mg/mL	0.1
Mobile phase		H ₂ O/MeOH (90/10)
Detection wavelength	nm	254
Injection volume	μL	10
Column		Agilent Zorbax SB-C18
Column dimensions	mm	150 × 4.6
Particle size	μm	5
Porosity	Å	100
Flow rate	mL/min	1.0
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Porosity	Å	100
Flow rate	mL/min	1.0
Temperature	°C	30
Pressure	MPa	10
Sample concentration	mg/mL	0.1
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Particle size	μm	5
Porosity	Å	100
Flow rate	mL/min	1.0
Temperature	°C	30
Pressure	MPa	10
Sample concentration		

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	CCGCTACCTG	GCCCTGGTGA	AAACCATGTC	CATGGGCCGG	ATGCGCGGCG	TGCGTGGGCG	CAAGCTCTAC
	AGCTTGGTGA	TCTGGGGGTG	TACGCTGCTC	CTGAGCTCAC	CCATGCTGGT	GTCCGGGACC	ATGAAGGAGT
	ACAGCGATGA	GGGCCACAAC	GTCACCGCTT	GTGTCATCAG	CTACCCATCC	CTCATCTGGG	AAGTGTTCAC
	CAACATGCTC	CTGAATGTCT	TGGGCTTCCT	GCTGCCCTG	AGTGTTCATCA	CCTTCTGCAC	GATGCAGATC
10	ATGCAGGTGC	TGCGGAACAA	CGAGATGCAG	AAGTTC AAGG	AGATCCAGAC	GGAGAGGAGG	GCCACGGTGC
	TAGTCTGGT	TGTGCTGCTG	CTATTTCATCA	TCTGCTGGCT	GCCCTTCCAG	ATCAGACCTC	TCCTGGATAC
	GCTGCATCGC	CTCGGCATCC	TCTCCAGCTG	CCAGAGCAGG	CGCATCATCG	ATGTAACTCAC	ACAGATCGCC
	TCCTTCATGG	CCTACAGCAA	CAGTGCCTC	AACCCATGG	TGTACGTGAT	CGTGGGCAAG	CGCTTCCGAA
	AGAAGTCTTG	GAGAGGTGTAC	CAGGGAGTGT	GCCAGAAAGG	GGGCTGCAGG	TCAGAACCCA	TTCAGATGGA
15	GAACTCCATG	GGCACACTGC	GGACCTCCAT	CTCCGTGGAA	CGCCAGATTG	ACAAACTGCA	GGACTGGGCA
	GGGAGCAGAC	AGTGAGCAAA	CGCCAGCAGG	GCTGCTGTGA	ATTTGTGTAA	GGATTGAGGG	ACAGTTGCTT
	TTCAGCATGG	GCCCAGGAAT	GCCAAGGAGA	CATCTATGCA	CGACCTTGGG	AAATGAGTTG	ATGTCTCCGG
	TAAAACACCG	GAGACTAATT	CCTGCCTGTC	CCAATTTTGC	AGGGAGCATG	GCTGTGAGGA	TGGGGTGAAC
	TCACGCACAG	CCAAGGACTC	CAAAATCACA	ACAGCATTAC	TGTTCTTATT	TGCTGCCACA	CCTGAGCCAG
20	CCTGCTCCTT	CCCAGGAGTG	GAGGAGGCCT	GGGGGACAGG	AGAGGAGTGA	CTGAGCTTCC	CTCCCGTGTG
	TTCTCCGTCC	CTGCCCCAGC	AAGACAACCT	AGATCTCCAG	GAGAACTGCC	ATCCAGCTTT	GGTGCAATGG
	CTGAGTGCAC	AAGTGAATTG	TTGCCCTGGG	TTTCTTTAAT	CTATTACAGT	AGAACTTTGA	AGGACAATTT
	CTTGCAATTAA	TAAAGGTTAA	GCCCTGAGGG	GTCCCTGATA	ACAACCTGGA	GACCAGGATT	TTATGGCTCC
	CCTCACTGAT	GGACAAGGAG	GTCTGTGCCA	AAGAAGAATC	CAATAAGCAC	ATATTGAGCA	CTTGCTGTAT
25	ATGCAGTATT	GAGCACTGTA	GGCAAGAGGG	AAGAAAGAGA	AGGAGCCATC	TCCATCTTGA	AGGAACTCAA
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	CCTGCCTC	CTGCAGAAAA	CAGCCTGAGC	TCCACCTCGG	CTTCTCCTTG	CCCTGGCTGG	TTGTCTCTAA
	CCCCTGTCTC	CTTCTGGACC	AGTTTTTGTC	CTTCCCTTGT	GACCTTGAGG	GGTAACAGCC	CTTTTCCAC
30	TTTCTTTCAG	CGCCGACATG	CTCAATGTCA	CCTTGCAAGG	GCCCACTCTT	AACGGGACCT	TGCCCAGAG
	CAAAATGCCCC	CAAGTGAGAGT	GCTGTGGGCTG	GCTCAACACC	ATCCAGCCCC	CCTTCTCTCTG	GGTGCTGTTT
	GTGCTGGCCA	CCCTAGAGAA	CATCTTTGTC	CTCAGCGTCT	TCTGCCTGCA	CAAGAGCAGC	TGCACGGTGG
	CAGAGATCTA	CCTGGGGAAC	CTGGCCGCAG	CAGACCTGAT	CCTGGCCTGC	GGGCTGCCCT	TCTGGGCCAT
	CACCATCTCC	AACAACCTCG	ACTGGCTCTT	TGGGGAGACG	CTCTGCCGCG	TGGTGAATGC	CATTATCTCC
35	ATGAACCTGT	ACAGCAGCAT	CTGTTTCTTG	ATGCTGGTGA	GCATCGACCG	CTACCTGGCC	CTGGTGA AAA
	CCATGTCCAT	GGGCCGGATG	CGCGGCGTGC	GCTGGGCCAA	GCTCTACAGC	TTGGTGATCT	GGGGGTGTAC
	GCTGCTCCTG	AGCTCACCCA	TGCTGGTGTT	CCGGACCATG	AAGGAGTACA	GGCATGAGGG	CCACAACGTC
	ACCGCTTGTT	TCATCAGCTA	CCATCCCTC	ATCTGGGAAG	TGTTACCAA	CATGCTCCTG	AATGTCGTGG
	GCTTCTCTGCT	GCCCTGAGT	GTCATCACCT	TCTGCAGCAT	GCAGATCATG	CAGGTGCTGC	GGAAACAACGA
40	GATGCAGAAG	TTCAAGGAGA	TCCAGACGGA	GAGGAGGGCC	ACGGTGCTAG	TCCTGGTTGT	GCTGCTGCTA
	TTCATCATCT	GCTGGCTGCC	CTTCCAGATC	AGCACCTTCC	TGGATACGCT	GCATCGCCTC	GGCATCCTCT
	CCAGCTGCCA	GGACGAGCGC	ATCATCGATG	TAATCACACA	GATCGCCTCC	TTCATGGCCT	ACAGCAACAG
	CTGCCTCAAC	CCACTGGTGT	ACGTGATCGT	GGGCAAGCGC	TTCGAAAGAA	AGTCTTGGA	GGTGTACCAG
	GGAGTGTGCC	AGAAAGGGGG	CTGCAGGTCA	GAACCCATTG	AGATGGAGAA	CTCCATGGGC	AACTGCGGGA
45	CCTCCATCTC	CGTGGAACGC	CAGATTCA	AACTGCAGGA	CTGGGACAGG	AGCAGACAGT	GAGCAAAACG
	CAGCAGGGCT	GCTGTGAATT	TGTGTAAGGA	TTGAGGGACA	GTTGCTTTTC	AGCATGGGCC	CAGGAATTGCC
	AAGGAGACAT	CTATGCACGA	CCTTGGGAAA	TGAGTTGATG	TCTCCGTTAA	AACACCGGAG	ACTAATTCTT
	GNCTTGCCCA	ATTTTGACAG	GAGCATGGCT	GTGAGGATGG	GGTGAACCTA	CGCACAGCCA	AGGACTCCAA
	AATCACAACA	GCATTACTGT	TCTTATTTGC	TGCCACACCT	GAGCCAGCCT	GCTCCTTCCC	AGGAGTGGAG
50	GAGGCCTGGG	GGCAGGGAGA	GGAGTGACTG	AGCTTCCCTC	CCGTGTGTTT	TCCGTCCCTG	CCCCAGCAAG
	ACAACCTAGA	TCTCCAGGAG	AACTGCCATC	CAGCTTTGGT	GCAATGGCTG	AGTGCAACAAG	TGAGTTGTTG
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	CTGAGGGGTC	CCTGATAACA	ACCTGGAGAC	CAGGATTTTA	TGGCTCCCCCT	CACTGATGGA	CAAGGGAGGT
	CTGTGCCAAA	GAAGAATCCA	ATAAGCACAT	ATTGAGCACT	TGCTGTATAT	GCAGTATTGA	GCACTGTAGG
55	CAAGAGGGAA	GAAAGAGAAG	GAGCCATCTC	CATCTTGAAG	GAACCTAAAG	ACTCAAGTGG	GAAACGACTGG
	CAGTGCCACC	ACCAGAAAGC	TGTTTCGACGA	GACGGTCGAG	CAGGGTGCTG	TGGGTGATAT	GGACAGCAGA
	AGGGGGAGAC	CAAGGTTCCA	GCTCAACCAA	TAACTATTGC	ACAACACACT	GTCCCTGCCT	CAGTTCCCTC
	TTCTGTAACA	TGAAGTCGTT	GTGAGGGTTA	AAGGCAGTAA	CAGGTATAAA	GTAAGTTAGAA	

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 15 GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT GCTGGCTGCC CTTCCAGATC
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TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC
CAGCACAGAG GGAGGGAGGG AGGGCAGGCA GCGGGGAGAA GTTCCCTGT GGTCTGTGGG AGTTGGGAAA
AGTTCCTTC CTTCCGGAGG GAGG -3' (FRAG. NO:2275) (SEQ. ID NO:3018)
25 5'- GAGCTCTTCA ATATTTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTTT
CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT CTGTCCCAA CTGGCAAGTC AGGAAACTCC
AGATTAAGGA GCCCAATGT GGTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG
AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC
TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGCTTGA TTGCTGGTTT GTAGGCTTGT
30 TATGAATCAA GTCACAGGGA AGAGGAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC
CCAGATCCAC TGGGCCCACT CTTATCTGTT CTCTTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAATG
TTTTGAAAGT CCCTGCCCTT TCCAGCTCCT ACCGTCTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT
AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC
TCCGAAGAAA CGGCCGCGTG TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC
35 ACTGTCGCCC TTGGGAGCCG TACGTGGCAT GACAAAGAAA TCCCAGGACT CCGCCTGCCC ACCTGGCCAC
CCTCTGTTA CACCTTCCGC GTAAACGCCC ACTGTTTACA TCCAAAATC AGACACAAAA TAACCACCTC
AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTTATT CACATGGGGC TTCCAGGCC
ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGTCCAC GACTCCAACG GGCAGCCGGG CCTACGCAA
CATGGAATC TTCCAAGAGC CTCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG
40 CCGCAGCCTT CCCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGCAGGAGT GCAGAGCTCA GCTGGAGGCG
AGGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG CCCTTCAAAG ATGAGCTGTT CCCGCCGCA
CTCCAGCTCT GGCTTCTGGG CTCCGAGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCCC
CGCAGTACCA GGGAGCGACT GAAGTGCCCA TGCCGCTTGC TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT
GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA
45 GCGGGGAGAA GTTCCCTGT GGTCTGTGGG AGTTGGGAAA AGTTCCTTC CTTCCGAGG GAGG-3'
(FRAG.NO:2275) (SEQ.ID NO:2461)
5'- GCCCTTCAAA GATGAGCTGT TCCGCGGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA
CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG
CTCCGAGAAA GGTGGGTGCC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAAGTCTC
50 CCAGCACAGA GGGAGGGAGG GAGGGCAGGC AGCGGGGAGA AGTTTCCCTG TGGTCGTGGG GAGTT -3' (FRAG.
NO:2275) (SEQ. ID NO:2460)
5'- GCCCTTCAAA GATGAGCTGT TCCGCGGCC ACTCCAGCTC TGGCTTCTGG GCTCCGAGGA GGGGTGGGGA
CGGTGGGGAC ATCAGGCTGC CCCGAGTAC CAGGGAGCGA CTGAAGTGCC CATGCCGCTT GCTCCGAGGA
AGGTGGGTGC CGGGCAGGGG CTGCTCCAGC CGCCTCACCT CTGCTGGGAG GACAACTGT CCCAGCACAG
55 AGGGAGGGAG GGAGGGCAGG CAGCGGGGAG AAGTTCCCT GTGGTCGTGG GGAGTT-3' (FRAG.NO:2275)(SEQ. ID
NO:2459)

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CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
CCTGAGCTCA CCCATGCTGG TGTTCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT
TGTGTCATCA GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC
5 TGCTGCCCT GAGTGTATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA
GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTATC
ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCTTGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT
GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG CCTACAGCA ACAGTGCCT
CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
10 TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCAGACTG CGGACCTCCA
TCTCCGTGGA ACGCCAGATT CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG
GGCTGCTGTG AATTGTGTGA AGGATTGAGG GACAGTTGCT T-3' (FRAG. NO:2275) (SEQ. ID NO:2458)
5'- ATGTCTCTC CTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCACC ACGGCTCTT
TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG ACCTTTGCCC AGAGCAAATG
15 CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG
GCCACCTAG AGAACATCTT TGTCTCAGC GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA
TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCTTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT
CTCCAACAAC TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC
CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
20 CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
CCTGAGCTCA CCCATGCTGG TGTTCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT
TGTGTCATCA GCTACCCATC CCTCATCTGG GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC
TGCTGCCCT GAGTGTATC ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA
GAAGTTCAAG GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTATC
25 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCTTGATA CGCTGCATCG CCTCGGCATC CTCTCCAGCT
GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG CCTACAGCA ACAGTGCCT
CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAGATGG AGAACTCCAT GGGCAGACTG CGGACCTCCA
TCTCCGTGGA ACGCCAGATT CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG
30 GGCTGCTGTG AATTGTGTGA AGGATTGAGG GACAGTTGCT T-3' (FRAG. NO:2275) (SEQ. ID NO:2458)
5'- TGATCTATC ACAACCTGAG AGTAGTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT CAAGGACGTT
AAGTAACTTC CCCAGCTCAC ACGGCTTATA AGTAAGGCAG CCAGGATGTG AACCCAGTAG GACTATCTGG
CTGCAAAGTC CCCACCCTCC CTCGCCATCT GTATCTCTCA ATCATCTTCA GTGCTTTGCT GATAGAAGGT
ACGGAATATC GATGCCACAG ACTGTCCAGG AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGTCTCCAA
35 GCCAGACTGG AATCTCCAGG TCTGGAATGA TATCATTTTT CTCTTTAAT AAATTAATC ACCCACCACA
CGGCTTTGAG AGGCTCAAAG GTGACCAACT CCCTTGGGAG GGCCCGGTT GATAAGGAAG GAATGTGAAT
CCTCCCATCA CGGAAGCTTC AAGGAGGTCA AGGGTCCAAC ACTTGAGATT GTTAGTGCTG TTGGTGGATA
CTGCAGAAAT TCCAGTGGAG CCTCAGATGA AGAACATGAG GCCCCGTTTA GATCCAAGGA TCAGAGGGGG
CTCTGTAAGA CCCAGGGGAG TCAGGTGCAC TGGAGCGCGG GCTGCAGAAA ACAGCTGAG CTCCACCTCG
40 GCTTCTCCTT GCCCTGGCTG GTTGTCCTTA ACCCTGTCT CCTTCTGGAC CAGT'TTTGT CTTTCCCTTG
TGACCTGAGG GGTAAACAGCC TCTTTTCCAC TTTCTTTTCA CGCCGACATG CTCAATGTCA CCTTGCAAGG
GCCACTCTT AACGGGACCT TTGCCAGAG CAAATGCCCC CAAGTGGAGT GGCTGGGCTG GCTCAACACC
ATCCAGCCCC CCTTCTCTG GTGCTGTTC GTGCTGGCCA CCTAGAGAA CATCTTTGTC CTCACGCTCT
TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA CCTGGGGAAC CTGGCCGAG CAGACCTGAT
45 CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC AACAACCTCG ACTGGCTCTT TGGGGAGACG
CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT ACAGCAGCAT CTGTTTCTCTG ATGCTGGTGA
GCATCGACCG CTACCTGGCC CTGGTGAATA CCATGTCCAT GGGCCGATG CGCGGCGTGC GCTGGGCCAA
GCTCTACAGC TTGGTGATCT GGGGGTGATC GCTGCTCCTG AGCTCACCCA TGCTGGTGTT CCGGACCATG
AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG TCATCAGCTA CCCATCCCTC ATCTGGGAAG
50 TGTTCACCAA CATGCTCCTG AATGTCGTGG GCTTCTGCT GCCCTGAGT GTCATACCT TCTGCACGAT
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ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTATCATCTC GCTGGCTGCC TCTCAGATC AGCACCTTCC
TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA
GATCGCCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC CCACTGGTGT ACGTGATCGT GGGCAAGCGC
55 TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC AGAAAGGGGG CTGCAGGTCA GAACCCATT
AGATGGAGAA CTCCATGGGC AACTGCGGA CCTCCATCTC CGTGAACGC CAGATTACA AACTGCAGGA
CTGGGACAGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT GCTGTGAATT TGTGAAGGA TTGAGGGACA
GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTGA
TGTCTCCGGT AAAACACCGG AACTAATTC CTGCCCTGCC CAATTTTCGA GGGAGCATGG CTGTGAGGAT
60 GGGGTGAAC CAGCACAGC CAAGGACTCC AAAATCACA CAGCATTACT GTTCTTATT GCTGCCACAC
CTGAGCCAGC CTGCTCCTTC CCAGGCTGG AGGAGGCTG GGGAGGGAG AGGAGTGACT GAGCTTCCCT
CCCGTGTGTT CTCCGCTCCCT GCCCCAGCAA GACAACCTAG ATCTCCAGGA GAACTGCCAT CCACGTTTGG

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TGCAATGGCT GAGTGCACAA GTGAGTTGTT GCCCTGGGTT TCTTTAATCT ATCAGCTAGA ACTTTGAAGG
ACAATTTCTT GCATTAATAA AGGTAAAGCC CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTT
ATGGCTCCCC TCACTGATGG ACAAGGAGGT CTGTGCCAAA GAAGAATCAA TAAGCACATA TGAGCACTTC
TGTATATCAG TATTGAGCAC TGTAGGCA -3' (FRAG. NO:2275) (SEQ. ID NO:2456)

5 5'- CTGCAGAAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCCTGGCTGG TTGTCCTTAA CCCCTGTCTC
CTTCTGGACC AGTTTTTGTG CTTCCCTTGT GACCCTGAGG GGTAACAGCC TCTTTTCCAC TTTCTTTCAG
CGCCGACATG CTCAATGTCA CCTTGCAAGG GCCCACTCTT AACGGGACCT TTGCCAGAG CAAATGCCCC
CAAGTGGAGT GGCTGGGCTG GCTCAACACC ATCCAGCCCC CCTTCCTCTG GGTGCTGTTC GTGCTGCCCA
CCCTAGAGAA CATCTTTGTC CTCAGCGTCT TCTGCCTGCA CAAGAGCAGC TGCACGGTGG CAGAGATCTA
10 CCTGGGGAAC CTGGCCGAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGGCCAT CACCATCTCC
AACAACCTCG ACTGGCTCTT TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT
ACAGCAGCAT CTGTTTCCTG ATGCTGGTGA GCATCGACCG CTACCTGGCC CTGGTGAAAA CCATGTCCAT
GGGCCGGATG CGCGGCGTGC GCTGGGCCAA GCTCTACAGC TTGGTGATCT GGGGGTGATG GCTGCTCCTG
AGCTCACCCA TGCTGGTGTG CCGGACCATG AAGGAGTACA GCGATGAGGG CCACAACGTC ACCGCTTGTG
15 TCATCAGCTA CCCATCCCTC ATCTGGGAAG TGTTACACAA CATGCTCCTG AATGTCGTGG GCTTCTGCT
GCCCCTGAGT GTCATCACCT TCTGCACGAT GCAGATCATG CAGGTGCTGC GGAACAACGA GATGCAGAAG
TTCAAGGAGA TCCAGACGGA GAGGAGGGCC ACGGTGCTAG TCCTGGTTGT GCTGCTGCTA TTCATCATCT
GCTGGCTGCC CTTCCAGATC AGCACCTTCC TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA
GGACGAGCGC ATCATCGATG TAATCACACA GATCGCCTCC TTCATGGCCT ACAGCAACAG CTGCCTCAAC
20 CCACTGGTGT ACGTGATCGT GGGCAAGCGC TTCCGAAAGA AGTCTTGGGA GGTGTACCAG GGAGTGTGCC
AGAAAGGGGG CTGCAGGTCA GAACCCATTC AGATGGAGAA CTCCATGGGC AACTGCGGA CCTCCATCTC
CGTGGAACGC CAGATTCACA AACTGCAGGA CTGGGCAGGG AGCAGACAGT GAGCAAACGC CAGCAGGGCT
GCTGTGAATT TGTGTAAGGA TTGAGGGACA GTTGCTTTTC AGCATGGGCC CAGGAATGCC AAGGAGACAT
CTATGCACGA CCTTGGGAAA TGAGTTGATG TCTCCGGTAA AACACCGGAG ACTAATTCCT GNCCTGCCCA
25 ATTTTGCAGG GAGCATGGCT GTGAGGATGG GGTGAACCTA CGCACAGCCA AGGACTCCA AATCACACA
GCATTACTGT TCTTATTTGC TGCCACACCT GAGCCAGCCT GCTCCTTCCC AGGAGTGGAG GAGGCTGGG
GGCAGGGAGA GGAGTGACTG AGCTTCCCTC CCGTGTGTTT TCCGTCCCTG CCCAGCAAG ACAACTTAGA
TCTCCAGGAG AACTGCCATC CAGCTTTGGT GCAATGGCTG AGTGCACAAG TGAGTTGTTG CCCTGGGTTT
CTTTAATCTA TTCAGCTAGA ACTTGAAGG ACAATTTCTT GCATTAATAA AGGTTAAGCC CTGAGGGGTC
30 CCTGATAACA ACCTGGAGAC CAGGATTTTA TGGCTCCCTT CACTGATGGA CAAGGGAGGT CTGTGCCAAA
GAAGAATCCA ATAAGCACAT ATTGAGCACT TGCTGTATAT GCAGTATTGA GCACTGTAGG CAAGAGGGAA
GAAAGAGAAG GAGCCATCTC CATCTTGAAG GAACTCAAAG ACTCAAGTGG GAACGACTGG CACTGCCACC
ACCAGAAAGC TGTTGACGA GACGGTCGAG CAGGGTGCTG TGGGTGATAT GGACAGCAGA AGGGGGAGAC
CAAGGTTCCTA GCTCAACCAA TAACTATTGC ACAACCACT GTCCCTGCCT CAGTTCCTC TTCTGTAACA
35 TGAAGTCGTT GTGAGGGTTA AAGGCAGTAA CAGGTATAAA GTACTTAGAA AAGCAAAGGG TGCTACGTAC
ATGTGAGGCA TCATTACGCA GACGTAACCT GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGA -3'
(FRAG. NO:2275) (SEQ. ID NO:2455)

5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTTAAA ATGAATGCTT TAAGCCGGGT GCAGTGCCTC
ACATCTGTAA TCCCAGCACT TTGGAGCCGA GCGGGTGGAT TGTGTGAGGT CAGGAGTTCG AGACCAACCT
40 GGCCAACATG GCAAAACCTC ACTCTTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG
TGATCCCAGC TACTCAGGAG GCTGAGACAG GAGAATCGCT TGAACCCGGG AGGCAAGGTT GCAGTGAGCC
AAGATTACGC CATTGTACTC CAGCCTGGGT GACAGAGAGA GACTCCGTCT CAAAAAATAA AAAAAAATAA
AAAAAATTAC GCTTCAAACA CATGATCTCT CACCACTGTT GAATTTTCTT TCTATGAGCC CAGGAGGGCC
TCTCAGAGAG GAAAGCTCCT AGGTCTTCCT TTCCCTCTGC AAATCTCCCTG CCTTGAAGGT TCAGAAGGAC
45 TGTGCGTGCT CGTTGCATCC TTTGCAAGTG TCCAAACCCT GATCCAGCT GTGCTTAGGG GTTCTGCAA
ACCTTTTCCA GGTGTTAATT ACCTCCCACT TCATTTCTCTG TTTACCAACT CAGCTTTTTG TTTTAGTGTG
TTTGAATTCC CTGAACCTGAC CGTTGTCTGA TCTCCACCTC CCAACTGAAT TAGGGGAGCT GGGCTTCTGG
AAACCCAGGT GCCGGGTGTT GCAGAGTGGC TGAAAGCTGG GATGTGGCAG ATCCGTGGCT ACATTCATGC
ACACACACAC ACCCACATAC CCACACATGC ACACACACAC ACACACCCGC ACTCACACAG TTGGACATGC
50 ATAGACCACA GCTTTCCACA CCCTTCCTAG ACAGGGGTCA CTTGGTATCC TGGAGAGAGT GTGAAGTCTC
GGAATGGAAA GAGGGGGGAT TAAGCCCCAC CTCTAGCCAT GGGACTGAGA CAAGCTACCA CCAACCATC
TGCGCCTTGT TTACCTCCTC TGTGAGGCAA GCACAGAGCC CATGCCTGCC CCCCTGGATG GGAGTGATGT
GAAACTTGAA GGGCGGTCAG AGCAAGGGTC GGGAATGGAA GGCCCTTGGG AAAAAAGGCC CTTTCAACTA
GGGGCACAGA GGAGGCCCTG GGCTGAGAAC TTGACAGCAC CTTGTAATTG GTAAGCCAAG CCCGAAGGGA
55 CTGGAATAC TCAGATGTGT CTGTCTCCTT TATTAGGTTT AAAGTCCCTC AAGACCCTGT CTCCATCACA
GTGCTCCAGT CCAGACCCCT CCTCTGAGCT CCAGACCCCTG CTGGACCCAA CCAGCCCTAT GGGGTGCGAT
CCCCACCTGC CTGGAATTCT CCAAAGAACC TCCCTTTTAA CAGTTCAGC CTTTAACAGT TCCAGTCTAA
ACACATGACC TTTCTCCTCT AAATCAGCCG CCCATCTCTG CCTTTGCAGG AGATGGAAGC CATGACACCT
GCCTCGCCCC TGTCCTCACC CCATCCATCT CCAATCAAGC ACTAGGCATG TCAGGTTTAC CCTCTAACT
60 CCTCTGGAAT CCACTCTCTC AGTCTCCATC ATCCCAAGTC GAAGCTAATG GGCTAACTGG TCCTTGCTTC
CACTCTACCC CCACTGCAGT CCTGACTTCC TGAGCAGCAG CCAGGGCCTA ATCGATATTC ACACCAAGCG
CCAACCTGAC TGAGATATCC TCCTGCACCA TCATCCCTCC ACCCTGTTTA GTTCTGCTCA CCCTCAGTGT

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	TCTCATCAAT	AATCCACTCC	CCTCACAGGC	GCGTTTGGGA	CCCCATGTTT	TATGCTCTCA	CAGGACCTTT
	TGCTTGATTT	TTCAGTGTAC	TTAGGTCAGT	TTGCAGTTAT	TAAGTGACTG	AGCAATGTCT	GGCTTCTCCA
	GTAGACTGTC	AGCTCCTAGC	CATTGTATAC	CTAGACCCGC	TGTGTGGGAG	CACGTGACAA	ACGTCCAGTG
	AGTCAGGGAC	TCAGCAGTCT	CCATTCTCTC	GCCCTGCTGG	AGAATGCGTG	TATTTGGCAA	TCCCCAGCCC
5	CTGTGCCATC	TAACCATCTT	TTCTTCTCTG	TTACAGCCCAG	GTGTGGCCTC	ACTCACATCC	CACTCTGAGT
	CCAAATGTTT	TCTCCCTGGA	AGATATCAAT	GTTTCTGTCT	GTTCGTGAGG	ACTCCGTGCC	CACCACGGCC
	TCTTTTCAGGT	GAGTCAAAGG	GATTCTCTCAG	TTCACTAGTT	AGGGGAGGTG	GGCAGACACC	CTGGAGAAGT
	CCCTGGAAAA	CTCAACTCTC	ATGCCCCGGA	CAACAGTTGA	AGGAACCATG	GTGATGTTAA	GCCCAAAGAC
	AAAACCTCTC	AGGTGTCCAA	GTCCCTGTTG	GAATCTTGGG	AGCAGAGGGA	ATGTTCTGTG	GTCTAGAGGA
10	AGAGGGGCTC	AGGGAGGAGA	AGGGCACATT	CCTGGTTGTT	ATATGTTTCT	ATCTATCCCA	GATGAAGTTG
	GAAGTGAAGG	GAAGAGAGTT	AAACATTAAA	GTAATAACCC	AGTGGATCAG	ACAGCAATGT	GCCAGATTGC
	CTTGGAACA	AAATATCTCC	AACACATGGC	TGACATTGGG	TGGGAGATCA	GAACACCTTA	AAGAGAGAAT
	TTAAGGGGAG	GGGGAGGAGG	ACCTGAGCCA	GAGTAGAAGC	AGAGGATAGG	GAGATCTGTT	CTTGGGGACA
	GCATTTGCAA	GAAACAAGGC	TGAGGGGTCC	ACTCCAACCT	CTCCACCCTG	CTGCAGGTGC	TGCCTATGAT
15	GAAGATGAGC	AGATGGCCAT	CTCAGCTGGG	GCCACAGTGC	ACTGGACCTA	TAGTTTCCAA	TTCCGCACTC
	AGCAGGCATC	TTTCTGATGA	TCCGATGGCT	TCTCAGAGCC	AGGGATGGGC	CAGGATCCAT	CCCCTTGGCT
	ACTGTCTTGC	TGAGAAATTT	ATAAGCAGCA	TCTGGTGCTA	TACTTTGGTC	TCTAGTGAGT	TAGCTCATGA
	AAGATGATAG	ACTCTCCAAG	CCAGGGGTAT	GCAGGAAATG	GGTTTCTGT	AGCTACAGAA	ATGGGGTTGA
	GGGTTGGACC	AAGGGACTAC	CCAGGGGAAG	TCTTACCTTC	AGAGGACTCT	GGAAAGGAGG	CTGCAAGTTT
20	TCATGGGTCA	AGAATTCAGA	GCCCAGTAGA	GACAGCTTAT	CTCTGTTCCA	AGATGTCTGG	GGCCTTGGTT
	GGAAGATTCA	AAGGCTAGGA	AACCAGGAGC	CACCAAAAGC	GTAACGGGGG	CCAGAGGATC	CACTTTCAAG
	GTGGCAAGTT	GGTTCCCCCC	ATGTGGCTGC	TTGAGTATCC	TCACATGGCG	GCTCACATCC	TTCCAAGTAA
	GCAATGCAAA	AGGCCAAGAA	AGATGCTGCA	AAGATGTTAT	GACCTAGCCT	CAGAAATCAC	ACACCATCCC
	TGCCACCATT	AGTAAGAAGT	CCAGCCCCAG	TCCAGGAGAA	GAGGAAGCAG	ATTCCTCCTT	TTGAAATGAA
25	GAATATCAAG	TAATTCGGGG	GGCATATGAA	AGCCACCACA	CACCACAGGG	ATCTTTTAG	AGCATACTTC
	TTATACCATC	ACTGTAGTTC	CTTAAGACTC	AGGGGCAAAAG	CCTCACTTCC	TTAGCACCCA	GTGAAGACCA
	CGCTTACTCC	CTCACTCAAC	CTCTTGCTAC	TTCCCACCTC	TCCTGTCCAA	CATCTAGTGT	CACTTTCCAG
	AACATACCAA	CAGCTTCCCC	AGTTCTGTGC	CTCTGCTCAG	GCTGTTCCCC	CTGCCTGGTC	CACTTGTCTT
	CCTTCTTGTC	CGGTCAAAAT	GCTTCTTATC	CTTCAAGACC	CAGCTCTAGA	GTCACCTCCA	ACCCCTTACC
30	CACCAGCCCC	CTCTCCAAGT	CTGTGTCCCA	CAACCCCCCT	GCTCCCTCCA	GGGCACCCTC	CACCCTCTGG
	GCCACAGTTG	TCAGGAGTCA	GGCAGGGCAG	GGGCCGGGTG	GTGTCTTCTT	TGTGTTCTTG	CACTCAGGGC
	AGAGCTCAGC	ACAGAGCAGA	CGCTCAAAAA	ACATTTAAAG	GATAGAAGCA	TTGATTTGTG	GGTCCCCCAG
	TCTGGCTCCA	GGATGCCAGC	CAGCTGCTCC	TAGAAGCAAA	CGGACTTTTC	CTGGGAAATC	CCAGAGGTGA
	TGATCAGTAA	TCTCTCCCGT	GACTCGTAGT	TCAGTCTTTC	CTCCATGAGC	CTGACTATCA	GTGGACCTTC
35	CAGAAAGAGC	CCCTTTCTCT	TCTCTCACCC	ACAGCACAGG	GCACCTGGGA	AATGCCCAAT	GAGTCTGCC
	TCTGGGTTGT	GCTTTGGACT	TTTCAGTGTG	TCTCGCATCC	ACTCTTCAAC	TTGAATGTTG	CAACAGCCAT
	GAAAAAAGAA	ATGCAAAGCG	ATTCAGGATG	AGAGCAATAC	CCTACTCCAA	AGAAGGCAAC	ATAGAAGCTC
	AGAGAGATCA	AGCAATTTGC	CCAAGACCAC	ACAGCTAGGA	GTGGAATCA	TGGCTGTCCA	AGCCCCATGC
	CTCTGCTGAA	GGTAGAGATG	AATTACAGCA	ACAAGTCTAG	AAAGGTGCCT	GCCCTATGGT	CTGTGAGTCT
40	TGCCTAAGAA	TGAAAGAGGA	GCCAGTGGGT	TAAAGATGAG	GTCACCAACA	ACGGTGGTGT	TGGAGTTTAC
	CACTGATAAT	AAGGGTGCAA	AATGTAAATT	ACTAATGTTT	ATTGAGCCTA	GTGCAGTGCG	TGGGGCATT
	TGCACATTGT	CTCTGATCCC	TATGACAACC	CTGAGAGGTA	GTGGTTTAA	CTGCCATGTT	ACAGGTGAGG
	TCATTGTGGT	TCAAGGACGT	TAAGTAACTT	CCCCAGCGTG	ACACGGCTTA	TAAGTAAGGC	AGCCAGGATG
	TGAACCCAGT	AGGACTATCT	GGCTGCAAAG	TCCCCACCCC	CCTCGCCATC	TGTATCCTCC	AATCACTTCA
45	GTGCTTTGCT	GCATAGAAGG	TAACGGAAAT	CACGATGCCA	CAGACTGTCC	AGGAAGACAG	AAACTAGGCA
	GATGGGCTGG	CCATGGTCTC	CAAGCCAGAC	TGGAATCTCC	AGGTCTGGAA	TGATATCATT	TTTCTCTTTT
	AATAAATTAA	CTCACCCACC	ACACGGCTTT	GAGAGGCTCA	AAGTTGACCA	ACTCCCTTGG	GAGGGCCCCG
	GTTGATAAGG	AAGGAACGTG	AATCCTCCCA	TCACGGAAGC	TTCAAGGAGG	TCAAGGGTCC	AACACTTGAG
	ATTGTTAGTG	CTGTTGGTGG	ATACTGGCCA	AGGAAATATC	CCAGTGAGGC	CTCGAGATGA	AGAACATGAG
50	GCCCCCGTTT	AGAACCAAGG	ATCAGAGGGG	GCTCTGTAAG	ACCCAGGGGA	GTCAGGTGCA	CTGGAGCGCG
	GGCATGCAGA	AAACAGCCTG	AGCTCCACCT	CGGCTTCTCC	TGTCCTTGGC	TGGTTGTCTT	TAACCCCTGT
	CTCCTTCTGG	ACCAGTTTTT	GTCCTTCCCT	TGTGACCGCT	GAGGGGTAAC	AGCCTCTTTC	CACTTTCTTT
	CAGCGCCGAC	ATGCTCAATG	TCACCTTGCA	AGGGCCCACT	CTTAACGGGA	CCTTTGCCCA	GAGCAAATGC
	CCCCAAGTGG	AGTGGCTGGG	CTGGCTCAAC	ACCATCCAGC	CCCCCTTCTC	CTGGGTGCTG	TTCTGTCTGG
55	CCACCCTAGA	GAACATCTTT	GTCTCTAGCG	TCTTCTGCCT	GCACAAGAGC	AGCTGCACGG	TGGCAGAGAT
	CTACCTGGGG	AACCTGGCCG	CAGCAGACCT	GATCCTGGCC	TGCGGGCTGC	CCTTCTGGGC	CATCACCATC
	TCCAACAAC	TCGACTGGCT	CTTTGGGGAG	ACGCTCTGCC	GCGTGGTGAA	TGCCATTATC	TCCATGAACC
	TGTACAGCAG	CATCTGTTTC	CTGATGCTGG	TGAGCATCGA	CCGCTACCTG	GCCCTGGTGA	AAACCATGTC
	CATGGGCGCG	ATGCGCGGCG	TGCGCTGGGC	CAAGCTCTAC	AGCTTGGTGA	TCTGGGGGTG	TACGCTGCTC
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	GTGTCATCAG	CTACCCATCC	CTCATCTGGG	AAGTGTTCAC	CAACATGCTC	CTGAATGTCG	TGGGCTTCTT
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	AAGAAAGAGA	AGGAGCCATC	TCCATCTTGA	AGGAACCTAA	AGACTCAAGT	GGGAACGACT	GGGCACTGCC
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	AAAAAAA -3' (FRAG. NO:2275) (SEQ. ID NO:2453)						
	5'- GAGCTCTTCA	ATATTTTAGT	GAAAGCTATA	GATGAGGCTC	CATAGGGGAT	AAAGCACAGA	CACACCTTTT
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 (FRAG..NO:2275) (SEQ.ID NO:2452)
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004040" 5294560

5'- TGATCCTATC ACAACCTGAG AGTAGTTTTT ACTCCATTTA CAGGTGAGGT CATTGTGGTT CAAGGACGTT
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35	5'-CAGATTCA TGTGTAAGGA CCTTGGGAAA GAGCATGGCT TCTTATTTGC GGAGTGACTG AACTGCCATC TTCAGCTAGA ACCTGGAGAC TAAGCACATA AGCCATCTCC TGTTTCGACG GCTCAACCAA GTGAGGGTTA TCATTACGCA GGAGCAGAAT TGGCTCCCTT AGAAGGCCAT AGGATCACAG GGACTGTTCC ATGAGCCCTA TTCACCTGAT TAGAACCTGG TAGAGAAGCT ACCTGGAGGG GCTAGAACCT AGAAGGGCTA AGAACCTGGA	AACGACAGGA TTGAGGGACA TGAGTTGATG GTGAGGATGG TGCCACACCT AGCTTCCCTC CAGCTTTGGT ACTTTGAAGG CAGGATTTTA TTGAGCACTT ATCTTGAAGG GACGGTCGAG TAACCTATTG AAGGCAGTAA GACGTAACTG CAGTATTGGG CCACCTGTCA GTCTTCAAAG TGCTGAGACC TGTCTCAGCA GAAGAGTGTG AAATGAATAT AGGGCTAGAA AAAACCTGAG CTGGAATCTG GGAGGGCTGG GAACCTGGAG GGGCTAGAAC	CTGGGCAGGG AGCAGACAGT AGCAGACAGT GAGCAAAACGC CAGCAGGGCT GCTGTGAATT TGTGCTTTTC TCTCCGGTAA GGTGAACCTA GAGCCAGCCT CCGTGTGTTC GCAATGGCTG ACAATTTCTT TGGTCCCCCT GCTGTATATG AACTCAAAGA CTCAAGTGGG CAGGGTGCTG TGGGTGATAT GTCCCTGCCT GTACTTAGAA GGATATGTTT AGCCGGTGGC TTCCCAACCAC TCTGATTTGT CCCCACCACC ACCAAGGGAT AAAAGGAATG TTATTAGCTG CCTGGAGAGG CTAGAAGCTG GAGAGCTAGA AATCTGGAGA GGCTAGAACC CTGGAAGGGC	AGCAGACAGT GAGCAAAACGC CAGCAGGGCT GCTGTGAATT AGCATGGGCC AACACCGGAG CGCACAGCCA GCTCCTTCCC TCCGTCCCTG AGTGACAAAG GCATTAATAA CACTGATGGA CAGTATTGAG CTCAAGTGGG TGGGTGATAT GTCCCTGCCT GTACTTAGAA ACTATAAGGA GGTGTGAAGC CCTGAGGCC GATGAGGCAG AGCCGGTACC TGTTCTGTCT GCAATGGTGT GTTGGAGAGC CTAGAACCAA GAGGACTAGA ACCTGGAGGG GCTAGAACCT TGGCAGGTTA TAGAACCTGT	CAGGAATGCC ACTAATTCCCT AGGACTCCAA AGGAGTGGAG AGGAGTGGAG TGAGTTGTTG AGGTTAAGCC CAAGGAGGTC CACTGTAGGC AACGACTGGG GGACAGCAGA CAGTTCCCTT AAGCAAAGGG AAAGACACTG ACCAAGTGTCT CAACCGCCAC AGGAAGATAT TGGGAAGGGG AATCAATGGT TCACCATCGG TAGAACCTGG GAAGGGCTAG ACCTGGAGGG CTAGAACCTG GGAGGGCTAG GAACCTAGAA AGAGCTAGAA	AAGGAGACAT GCCCTGCCCA AATCACAACA GAGGCCTGGG ACAACTTAGA CCCTGGGTTT CTGAGGGGTC TTTGCCAAAG AAGACCCAAG CACTGCCACC AGGGGGAGAC TTATGTAACA TGCTACGTAC AGGTCTAGAA GGCACACAGT ACACACAGGA TTCTAATCGG GAGAGTGCAG TTATTGGAAG CAGTGCCAGG AGAGCTAGAA AACCTGGAGG CTGGAATCTG GAGGGCTAGA AACCTGGAGG GGGCTAGAAC CATGGAGAGC	CTATGCACGA ATTTTGCAGG GCATTACTGT GGGAGGGAGA TCTCCAGGAG CTTTAATCTA CCTGATAACA AAGAATCCAA AAGAGGAAGG ACCAGAAAAGC CAAGGTTCCA TGAAGTCGTT ATGTGAGGCA ATAGCTCCGT AGGTGCTCAT GCATTTGGAG TCTTGCCACG GCTGTCTCAG GTGGCCCACT GCAGCACTCA CCTGGAGAAC GGCTAGAACC AAGGGCTAGA ACCTAGAAGG GCTAGAACCT CTGGAGAGCC TAGAACCCGG

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 10 AAAAAAAAAA -3' (FRAG. NO:) (SEQ. ID NO 2431)
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 5'-GGTCCCGTTBBGBGTGGGCCC-3' (FRAG. NO:2277) (SEQ. ID NO:2290)
 5'-GCCAGCCAGCCACTCCACTTGGGGGC-3' (FRAG. NO:2278) (SEQ. ID NO:2291)
 5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGGC-3' (FRAG. NO:2279) (SEQ. ID NO:2292)
 15 5'-GGCCAGAGAGGGCAGCCCGCAGCCAGGATCAGGTCTGCTGCGGCC-3'(FRAG.NO:2280)(SEQ.ID NO:2293)
 5'-GGAGATAATGGCATTACCCACGCGGC-3' (FRAG. NO:2281) (SEQ. ID NO:2294)
 5'-GGCCAGCGCACGCCGCGCATCCGGCCC-3' (FRAG. NO:2282) (SEQ. ID NO:2295)
 5'-GGGTCTGACCTGCAGCCCC-3' (FRAG. NO:2283) (SEQ. ID NO:2296)
 5'-GTCTCCTTGGCATTCTCTGGGCCC-3' (FRAG. NO:2284) (SEQ. ID NO:2297)
 20 5'-CAGTCACTCTCTCCCTGCCCCC-3' (FRAG. NO:2285) (SEQ. ID NO:2298)
 5'-CTTGCTGGGGCAGGGACGG-3' (FRAG. NO:2286) (SEQ. ID NO:2299)
 5'-GGTGBCBTTGBGCBTGTGCGGCGC-3' (FRAG. NO:2287) (SEQ. ID NO:2300)
 5'-GGTCCCGTTBBGBGTGGGCCC-3' (FRAG. NO:2288) (SEQ. ID NO:2301)
 5'-GCCAGCCAGCCACTCCACTTGGGGGC-3' (FRAG. NO:2289) (SEQ. ID NO:2302)
 25 5'-GGGTGGCCAGCACGAACAGCACCCAGAGGAAGGGGGGC-3' (FRAG. NO:2290) (SEQ. ID NO:2303)
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 5'-GGAGATAATGGCATTACCCACGCGGC-3' (FRAG. NO:2292) (SEQ. ID NO:2305)
 5'-GGCCAGCGCACGCCGCGCATCCGGCCC-3' (FRAG. NO:2293) (SEQ. ID NO:2306)
 5'-GGGTCTGACCTGCAGCCCC-3' (FRAG. NO:2294) (SEQ. ID NO:2307)
 30 5'-GTCTCCTTGGCATTCTCTGGGCCC-3' (FRAG. NO:2295) (SEQ. ID NO:2308)
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 5'-CCGTGTTGTCBGTGGTGCTG-3' (FRAG. NO:2298) (SEQ. ID NO:2311)
 5'-CCCGTTTGBGGTBTGGC-3' (FRAG. NO:2299) (SEQ. ID NO:2312)
 35 5'-GCTCCBCCBTTCCCTTTTCTCC-3' (FRAG. NO:2300) (SEQ. ID NO:2313)
 5'-TTGTTTTCCGTTTCTCTG-3' (FRAG. NO:2301) (SEQ. ID NO:2314)
 5'-CCGTCTGTGGTT-3' (FRAG. NO:2302) (SEQ. ID NO:2315)

β2 Adrenergic Receptor Kinase Nucleic Acids and Antisense Oligonucleotide Fragments

- 5'- GCCCGCGCC CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA
 40 AGAGCAAGGC TACGCGGCC GCGCGGCCA GCAAGAAGAT ACTGCTGCCC GAGCCAGCA TCCGCAGTGT
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GCAGCACAAG ACCAAAGACA AGCATGAGAT CGACCGCATG ACGCTGACGA TGGCCGTGGA GCTGCCGAC
TCCTTCTCCC CTGAACTACG CTCCTGCTG GAGGGGTTGC TGCAGAGGGA TGTCAACCGG AGATTGGGCT
GCCTGGGCCG AGGGGCTCAG GAGGTGAAAG AGAGCCCTT TTTCCGCTCC CTGGACTGGC AGATGGTCTT
CTTGCAAG TACCCTCCCC CGCTGATCCC CCCACGAGG GAGGTGAACG CGGCCGACGC CTTCGACATT
40 GGCTCCTTCG ATGAGGAGGA CAAAAAGGA ATCAAGTTAC TGGACAGTGA TCAGGAGCTC TACCGCAACT
TCCCCCTCAC CATCTCGGAG CGGTGGCAGC AGGAGGTGGC AGAGACTGTC TTCGACACCA TCAACGCTGA
GACAGACCGG CTGGAGGCTC GCAAGAAAGC CAAGAACAAG CAGCTGGGCC ATGAGGAAGA CTACGCCCTG
GGCAAGGACT GCATCATGCA TGGCTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG TGGCAGCGGC
GGTACTTCTA CCTGTTCCCC AACCCTCG AGTGGCGGGG CGAGGCGGAG GCGCCGAGA GCCTGCTGAC
45 CATGGAGGAG ATCCAGTCGG TGGAGGAGAC GCAGATCAAG GAGCGCAAGT GCCTGCTCCT CAAGATCCGC
GGTGGGAAAC AGTTCATTTT GCAGTGCAT AGCGACCCTG AGCTGGTGCA GTGGAAGAAG GAGTGCGCG
ACGCCTACCG CGAGGCCAG CAGCTGGTGC AGCGGGTGCC CAAGATGAAG AACAAGCCGC GCTCGCCCGT
GGTGGAGCTG AGCAAGGTGC CGCTGGTCCA GCGCGGACGT GCCAACGGCC TCTGACCCGC CCACCCGCT-3'
(FRAG. NO:) (SEQ. ID NO:2428)

50 **CCR-2 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-CTTTGTGAAG AAGGAATTGG CAACACTGAA ACCTCCAGAA CAAAGGCTGT CACTAAGGTC CCGCTGCCTT
GATGGATTAT AACTTGACC TCAGTGTGAC AACAGTGACC GACTACTACT ACCCTGATAT CTTCTCAAGC
CCCTGTGATG CGGAATTAT TCAGACAAAT GGCAAGTTGC TCCTTGCTGT CTTTATTGTC CTCCTGTTTG
TATTCAGTCT TCTGGGAAAC AGCCTGGTCA TCCTGGTCTT TGTGGTCTGC AAGAAGCTGA GGAGCATCAC
55 AGATGTATAC CTCTGAACC TGGCCCTGTC TGACCTGCTT TTTGTCTTCT CCTTCCCTT TCAGACATAC
TATCTGCTGG ACCAGTGGGT GTTGGGACT GTAATGTGCA AAGTGGTGTG TGGCTTTTAT TACATTGGCT
TCTACAGCAG CATGTTTTTC ATCACCCTCA TGAGTGTGGA CAGGTACCTG GCTGTTGTCC ATGCCGTGTA
TGCCCTAAAG GTGAGGACGA TCAGGATGGG CACAACCTGT TGCCTGGCAG TATGGCTAAC CGCCATTATG
GCTACCATCC CATTGCTAGT GTTTTACCAA GTGGCTCTG AAGATGGTGT TCTACAGTGT TATTATTTT
60 ACAATCAACA GACTTTGAAG TTGAAGATCT TCACCAACTT CAAAATGAAC ATTTTAGGCT TGTTGATCCC

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308

ACCAAGGCCA TCAGGTGGT GTCATTGTG GTCATTGCAT CTTTACTTTT CTGGGTCCCA TTCAACGTGG
TTCTTTTCCT CACTTCCTTG CACAGTATGC ACATCTTGA TGGATGTAGC ATAAGCCAAC AGCTGACTTA
TGCCACCCAT GTCACAGAAA TCATTCCTT TACTCACTGC TGTGTGAACC CTGTTATCTA TGCTTTTGTT
GGGAGAAGT TCAAGAAACA CCTCTCAGAA ATATTTCAGA AAAGTTGCAG CCAAATCTTC AACTACCTAG
5 GAAGACAAAT GCCTAGGGAG AGCTGTGAAA AGTCATCATC CTGCCAGCAG CACTCCTCCC GTTCCTCCAG
CGTAGACTAC ATTTTGTGAG GATCAATGAA GACTAAATAT AAAAAACATT TTCTTGAATG GCATGCTAGT
AGCAGTGAGC AAAGGTGTGG GTGTGAAAGG TTTCACAAAA AAGTTCAGCA TGAAGGATGC CGTGTGTGTT
GTTGCCAACA CTTGGAACAC AATGACTGGA GACATAGTTG TGCATGCCTG GCACAACATC AAGCCTGTGA
TTGTGTTTAT TGATGATGTT GAACAAGTGG TGGCTTTGAG GGATTCTGTA TGCCAAGTGG AAAAAAAGA
10 TGTCTCCGGA ATTCGACAGG TTATCA-3' (FRAG. NO:) (SEQ. ID NO:2462)

CAGTCCATGT CATCTACACA GTCAACCTCT ACAGCAGTGT CCTCATCCTG GCCTTCATCA GTCTGGACCG
 CTACCTGGCC ATCGTCCACG CCACCAACAG TCAGAGGCCA AGGAAGCTGT TGGCTGAAAA GGTGGTCTAT
 GTTGGCGTCT GGATCCCTGC CCTCCTGCTG ACTATTCCCG ACTTCATCTT TGCCAACGTC AGTGAGGCAG
 5 ATGACAGATA TATCTGTGAC CGCTTCTACC CCAATGACTT GTGGGTGGTT GTGTTCCAGT TTCAGCACAT
 CATGGTTGGC CTTATCCTGC CTGGTATTGT CATCCTGTCC TGCTATTGCA TTATCATCTC CAAGCTGTCA
 CACTCCAAGG GCCACCAGAA GCGCAAGGCC CTCAAGACCA CAGTCATCCT CATCCTGGCT TTCTTCGCCT
 GTTGGCTGCC TTAATACTT GGGATCAGCA TCGATCCTT CATCCTCCTG GAAATCATCA AGCAAGGGTG
 TGAGTTTGAG AACACTGTGC ACAAGTGGAT TTCCATCACC GAGGCCCTAG CTTTCTTCCA CTGTTGTCTG
 AACCCCATCC TCTATGCTTT CCTTGGAGCC AAATTTAAAA CCTCTGCCCA GCACGCACTC ACCTCTGTGA
 10 GCAGAGGGTC CAGCCTCAAG ATCCTCTCCA AAGGAAAGCG AGGTGGACAT TCATCTGTTT CCACTGAGTC
 TGAGTCTTCA AGTTTTCACT CCAGCTAACA CAGATGTAAA AGACTTTTTT TTATACGATA AATAACTTTT
 TTTAAGTTA CACATTTTTC AGATATAAAA GACTGACCAA TATTGTACAG TTTTATTGCT TTGTTGGATT
 TTTGTCTTGT GTTCTTTAG TTTTGTGAA GTTTAATTGA CTTATTATA TAAATTTTTT TTGTTTCATA
 TTGATGTGTG TCTAGGCAGG ACCTGTGGCC AAGTCTTAG TTGCTGTATG TCTCGTGGTA GGACTGTAGA
 15 AAAGGGAACCT GAACATTCCA GAGCGTGTAG TGAATCACGT AAAGCTAGAA ATGATCCCCA GCTGTTTATG
 CATAGATAAT CTCTCCATTC CCGTGAACG TTTTCTCTGT TCTTAAGACG TGATTGTGCT GTAGAAGATG
 GCACCTTATA CCAGGAGGTA AAGTGGTATA GAAATGTCTG TTTTTCAGTT TTCAGGAGTG GGTGATTTC
 AGCACCTACA GTGTACAGTC TTGTATTAAG TTGTAAATAA AAGTACATGT TAAACTTACT TAGTGTATG
 TTCTGATTTT TGTTGACATT CTTTGGCTA GTAGAAGACA AAAGTAATAC ATTTATGGTA TGCAAAAGCAC
 20 TATCCTAGGT ATTTCAATTG AATATTTTAC TTACCCCTTA TCACAACTCT GATAGATTCT GCTTCTGTGA
 CTAATTACAT TTTATAGAAG AGGAAACGGA GGCACAGAAA GCCTAAGTAA CTTGGTTAAA GGCATGTAGT
 AAGTATCAAA TCCTGTATTT TAAACCAGGT AACATGACTT AACGAATCTG AAGCCTTCAC CACTTTAAAT
 TCAAATGGAA GTTTAGAAAT GGCCAGCCAG CACCTATTTG TATGAAAGGT CATCTTTCAG AGGATAAGCA
 TGTATAAAGA AGAAAAGGTA TGCAGTCGTG TTTGGATTTT ACTCCACCAT C-3' (FRAG. NO.) (SEQ. ID NO: 2463)

25 **CD-34 Nucleic Acids and Antisense Oligonucleotide Fragments**

5'-AGGATGATGG TGATGGGGAA CTAAATGGGG AAATATGGAA GGTACAGGA AAAGTTAACA CAAGTTAGCA
 AAAGTTAAC ATAACACAAA AAGGTCTTGC AGGAAAAAAA AAAGAAAAGA AAAGAAAAGAA AAAGTCTCCA
 AGAATGGTTT GGACAGCCAA AATGAATACT TATAGTCACG TATACCTGCT CACTCCTGAC GCTTCACTCA
 30 CACACAGCAC AGGATCTGGT GAGGCTATCA TAAATGTGC CACATTGTGG TTAAGTTTAA CCTGATTAAC
 GAAATGCTCA CACTTCTAAA CTGAGGTCTT CAGATAGAT TCCTTTTGCA AGATTGTTAC TGGCTTACAA
 CTTAAAAATA AAGGAAAATC ACAAGGAAAG AAAAGTGGGG AAAAAATCGG AGGAAACTTG CCCCTGCCCT
 GGCCACCGGC AAGGCTGCCA CAAAGGGGTT AAAAGTTAAG TGGAAGTGGA GCTTGAAGAA GTGGGATGGG
 GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCGAA CAAACCTCCA CCTTTTTTGG CCTCGACGGC
 35 GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACAGGG GAGCTCAAGT TAGTAGCAGC
 CAAGGAGAGG CGCTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCCC
 ACCCTCTCC CGGGCGGAGG GGGCGGGAAG AGCGCGTCTT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT
 GCGTCTCTCT AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCCG
 CGGGGCTGGA CCGCGCTTGT CTGTCTGAGT TTGCTGC CCTTTTTTGG CCTCGACGGC GGCAACCCAG
 40 CCTCCCTCCT AACGCCCTCC GCCTTTGGGA CCAACAGGG GAGCTCAAGT TAGTAGCAGC CAAGGAGAGG
 CGTGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAAATA AGACCTCCAG CTGTGCGGAG TTTAAGAAGG
 CGGGCGGAGG GGGCGGGAAG AGCGCGTCTT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT GCGTCTCTCT
 AGGAGCCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGAGGGCCC AGGATGCCGC GGGGCTGGAC
 CGCGCTTTGC TTGCTGAGTT TGCTGCCTTC TGGGTTTCATG AGTCTTGACA ACAACGGTAC TGCTACCCCA
 45 GAGTTACCTA CCCAGGGAAC ATTTTCAAA GTTCTACAA ATGTATCCTA CCAAGAACTA ACAACACCTA
 GTACCTTGG AAGTACCAGC CTGCACCTGT TTTCTCAACA TGGCAATGAG GCCACAACAA ACATCACAGA
 AACGACAGTC AAATTCACAT CTACCTCTGT GATAACCTCA GTTTATGGAA ACACAAACTC TTCTGTCCAG
 TCACAGACCT CTGTAATCAG CACAGTGTTC ACCACCCAG CCAACGTTTC AACTCCAGAG ACAACCTTGA
 AGCCTAGCCT GTCACCTGGA AATGTTTCAG ACCTTTCAC CACTAGCACT AGCCTTGCAA CATCTCCAC
 TAAACCTAT ACATCATCTT CTCCTATCCT AAGTGACATC AAGGCAGAAA TCAAATGTTT AGGCATCAGA
 50 GAAGTAAAAT TGACTCAGGG CATCTGCCTG GAGCAAAATA AGACCTCCAG CTGTGCGGAG TTTAAGAAGG
 ACAGGGGAGA GGGCCTGGCC CGAGTGTCTG GTGGGGAGGA GCAGGCTGAT GCTGATGCTG GGGCCAGGT
 ATGCTCCCTG CTCCTTGCCC AGTCTGAGGT GAGGCCTCAG TGTCTACTGC TGGTCTTGGC CAACAGAACA
 GAAATTTCCA GCAAACTCCA ACTATGAAA AAGCACCAAT CTGACCTGAA AAAGCTGGGG ATCCTAGATT
 55 TCACTGAGCA AGATGTTGCA AGCCACCAGA GCTATTCCCA AAAGACCCTG ATTGCACTGG TCACCTCGGG
 AGCCTGTCTG GCTGTCTGG GCATCACTGG CTATTTCTGT ATGAATCGCC CAGACTGGAG CCCACAGGA
 GAAAGGGTGG GCGAAGACCC TTATTACACG GAAAAACGGT GAGGCCAGGG CTATAGCTCA GGACCTGGGA
 CCTCCCTGA GGCTCAGGGA AAGGCCAGTG TGAACCGAGG GGCTCAGAAA AACGGGACCG GCCAGGCCAC
 CTCCAGAAAC GGCCATTGAG CAAGACAACA CGTGGTGGCT GATACCGAAT TGTGACTCGG CTAGGTGGGG
 CAAGGCTGGG CAGTGTCCGA GAGAGCACCC CTCTCTGCAT CTGACCACGT GCTACCCCCA TGCTGGAGGT
 60 GACATCTCTT ACGCCCAACC CTTCCCCTT GCACACACCT CAGAGGCTGT TCTTGGGCCC CTACACCTTG
 AGGAGGGGGC AGGTAAACTC CTGCTCTTTA CACATTCCGC TCCCTGGAGC CAGACTCTGG TCTTCTTTGG
 GTAAACGTGT GACGGGGGAA AGCCAAGGTC TGGAGAAGCT CCCAGGAACA ATCGATGGCC TTGCAGCACT
 CACACAGGAC CCCCCTCCCC TACCCCTCC TCTCTGCCGC AATACAGGAA CCCCCAGGGG AAAGATGAGC
 TTTCTAGGC TACAATTTTC TCCCAGGAAG CTTTGATTTT TACCGTTTCT TCCCTGTATT TTCTTTCTCT

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Variable	Mean	SD
Age	34.5	10.2
Gender		
Male	1.2	1.0
Female	0.8	0.8
Marital status		
Married	1.5	1.0
Single	0.5	0.5
Education		
High school	1.0	1.0
College	0.5	0.5
Postgraduate	0.5	0.5
Occupation		
Managerial	1.0	1.0
Professional	0.5	0.5
Service	0.5	0.5
Unemployed	0.5	0.5
Income		
Low	1.0	1.0
Medium	0.5	0.5
High	0.5	0.5
Health status		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Stress level		
Low	1.0	1.0
Medium	0.5	0.5
High	0.5	0.5
Life satisfaction		
Satisfied	1.0	1.0
Dissatisfied	0.5	0.5
Work-life balance		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Family support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Community support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Workload		
Low	1.0	1.0
Medium	0.5	0.5
High	0.5	0.5
Work environment		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Work-life balance		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Family support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Community support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Workload		
Low	1.0	1.0
Medium	0.5	0.5
High	0.5	0.5
Work environment		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Work-life balance		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Family support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Community support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Workload		
Low	1.0	1.0
Medium	0.5	0.5
High	0.5	0.5
Work environment		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Work-life balance		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Family support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Community support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Workload		
Low	1.0	1.0
Medium	0.5	0.5
High	0.5	0.5
Work environment		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Work-life balance		
Good	1.0	1.0
Fair	0.5	0.5
Poor	0.5	0.5
Family support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Community support		
High	1.0	1.0
Medium	0.5	0.5
Low	0.5	0.5
Workload		
Low	1.0	1.0
Medium	0.5	0.5
High	0.5	0.5
Work environment		

TGCAATTAAA GTGATACTGA AACAC-3' (FRAG. No:_) (SEQ. ID NO:2465)

Eotaxin Antisense Nucleic Acids and Oligonucleotide Fragments

	5'-GCATTTTTC	AAGTTTATG	ATTTATTTAA	CTTGTGGAAC	AAAAATAAAC	CAGAAACCAC	CACCTCTCAC
	GCCAAAGCTC	ACACCTTCAG	CCTCCAACAT	GAAGGTCTCC	GCAGCACTTC	TGTGGCTGCT	GTCATAGCA
5	GCTGCCTTCA	GCCCCAGGG	GCTCGCTGGG	CCAGCTTCTG	TCCCAACCAC	CTGCTGCTTT	AACCTGGCCA
	ATAGGAAGAT	ACCCCTTCAG	CGACTAGAGA	GCTACAGGAG	AATCACCAGT	GGCAATGTG	CCCAGAAAGC
	TGTGATCTTC	AAGACCAAAC	TGGCCAAGGA	TATCTGTGCC	GACCCCAAGA	AGAAGTGGGT	GCAGGATTCC
	ATGAAGTATC	TGGACCAAAA	ATCTCCAAC	CCAAAGCCAT	AAATAATCAC	CATTTTGA	ACCAAACCAG
	AGCCTGAGTG	TTGCCTAATT	TGTTTTCCCT	TCTTACAATG	CATTCTGAGG	TAACCTCATT	ATCAGTCCAA
10	AGGGCATGGG	TTTTATTATA	TATATATATA	TTTTTTTTTT	AAAAAAAAC	GTATTGCATT	TAATTTATTG
	AGGCTTTAAA	ACTTATCCTC	CATGAATATC	AGTTATTTTT	AAACTGTAAA	GCTTTGTGCA	GATTCTTTAC
	CCCCTGGGAG	CCCCAATTCG	ATCCCCTGTC	ACGTGTGGGC	AATGTTCCCC	CTCTCCTCTC	TCCTCCCTG
	GAATCTTGTA	AAGGTCCTGG	CAAAGATGAT	CAGTATGAAA	ATGTCATTGT	TCTGTGAAC	CCAAAGTGTG
	ACTCATTTAA	TGGAAGTAAA	TGTTGTTTAA	GGAATAC	ATGAAGGTCT	CCGCAGCACT	TCTGTGGCTG
15	CTGCTCATAG	CAGCTGCCTT	CAGCCCCCAG	GGGCTCGCTG	GGCCAGCTTC	TGTCCCAACC	ACCTGCTGCT
	TTAACCTGGC	CAATAGGAAG	ATACCCCTTC	AGCGACTAGA	GAGCTACAGG	AGAATCACCA	TGGGCAATG
	TCCCCAGAAA	GCTGTGATCT	TCAAGACCAA	ACTGGCCAAG	GATATCTGTG	CCGACCCCAA	GAAGAAGTGG
	GTGCAGGATT	CCATGAAGTA	TCTGGACCAA	AAATCTCCAA	CTCCAAAGCC	ATAA	CCACATATTC
	CCAAGGCAAG	ATCCAGATGG	ATTAAAAAAT	GTACCAAGTC	CCTCCTACTA	GCTTGCCTCT	CTTCTGTTCT
20	GCTTGACTTC	CTAGGATCTG	GAATCTGGTC	AGCAATCAGG	AATCCCTTCA	TCGTGACCCC	CGCATGGGCA
	AAGGCTTCCC	TGGAATCTCC	CACACTGTCT	GCTCCCTATA	AAAGGCAGGC	AGATGGGCCA	GAGGAGCAGA
	GAGGCTGAGA	CCAACCCAGA	AACCACCACC	TCTCACGCCA	AAGCTCACAC	CTTCAGCCTC	CAACATGAAG
	GTCTCCGCAG	CACCTCTGTG	GCTGCTGCTC	ATAGCAGCTG	CCTTCAGCCC	CCAGGGGCTC	GCTGGGCCAG
	GTAAGCCCCC	CAACTCCTTA	CGGAAAAGGT	AAGGTAACCA	CCTCCAGGCT	ACTAGGTCAG	CAAGAATCTT
25	TACAGACTCA	CTGCAAATTC	TCCATTGAA	AAATAGGGAA	ACAGGTTTGG	TGGGTGGACA	AGAAATGCCT
	CAACCGTCAC	ATCCAGTCAC	TGGAAGAGCC	AGAACTAGAA	AGCTCCCGAG	TCITTTCCCC	ACATTCAGAA
	GGGCCGCTGG	GTGCATCCTT	ACCCAGCTAT	CCTTACAGTG	TTTGGGAATG	GGGAATGGCT	CTGTCTTACT
	GTGGGCATGG	TGGGCATTTT	TGGCAGTGGG	AGAGAAGGAA	AATCTGTTGA	TTAGAAGCTC	AGTATGTTAA
	TTCGACTCCA	GGACAGCTTT	CAGAGACAGT	GGCTAAGAGA	AGAACGAGGT	CCCAGGGGAT	CTCTTGAGGT
30	GACTTATTTT	GACACTCTTT	GGGAAAAGTTA	TCTAGGAGAT	TGTTCCATA	ACTCATTTTC	CCATACTCTG
	GTGACAAATT	TACTGAGTGT	ATCGGTCCCA	CTGAGCCAGT	GCATAGCATG	GTAACAAACA	GTTCTAAATT
	ATCAATGACT	TAACAGAATT	AACTAAATTA	ACAAAAGTTA	CTTTCTCACT	TGTACTAAAT	ATCTATAATG
	TATGGGCTCA	GGCTTCTGCA	TTTTATACTC	AGGATTCTAG	ACTGATGGAG	AAGTTGCCAT	GTGGGGGAAC
	ATTGATGGAT	ACTGTGATAA	AGCAGAAGAA	AGCTCTCAGG	AGTCTTGCAT	AGGCAATGCA	CTGTGGCTCA
35	AAAATGACAC	CCATCACTTT	GTCTCCTTCT	TTATTGATCA	AAACTAATTA	ATGCCTCCAA	CCAAACAAAA
	GTGGCCAAGA	AATGCAAGTC	TACCTTGTGT	CTCAAAACAG	AGGATGGAGA	ATATTTGGTG	AAAATTACCA
	TGACCATCAC	ATGGCCACGT	AGGTCTTTAT	AATGACAGAG	CTAGCATTTG	TCACATTGAC	CAAGCTTTGT
	CCATACACTC	TACAGTAATG	ATGAGTCCTC	AGTGCACAGG	GGAGGATGCT	GAAGACACAG	GACAGCATCC
	TCCAGACACA	TAAGACTTCA	GAGCAGAGGG	ATTCTCCCTC	CACCTCTCGC	AATTCCTTGC	TTTCTCCTAA
40	CTTCTTTTAC	AAAGTCATGC	TTGGAAATGT	CTATGTATCA	TCATGTGGCT	CATTTTTTTC	TCTGTTTATT
	TTTTTTCCCC	AAAATTCAGC	TTCTGTCCCA	ACCACCTGCT	GCTTTAACCT	GGCCAATAGG	AAGATACCCC
	TTACGCGACT	AGAGAGCTAC	AGGAGAATCA	CCAGTGGCAA	ATGTCCCCAG	AAAGCTGTGA	TGTAAGTAAA
	TAAAGTTTAC	CCTCCCCTAG	ACAAAAAAAT	AATGTCTAGG	GCACAGAGTC	AAGAAGCTGTG	GGAGTCATAG
	ACTCTGATAG	TTTGACCTCT	ATGGTCCAAT	TCATTAATTT	TCACAAGTGA	GTGTTCACTC	CCAGCTCCCT
45	GCCTGGGAGA	TTGCTGTAGT	CATATCAATT	TCTTCAAGTC	AAGAGCAAAG	ATGGTTTTAC	TGGGCCTTTA
	AGAGCAGCAA	CTAACCCAAG	AGTCTCATCC	TTCTCCTCT	CCGTAGCAAC	CCTTTGTCCA	GGGGCAGATG
	GTCCTTAAAT	ATTTAGGGTC	AAATGGGCAG	AATTTTCAAA	AACAATCCTT	CCAATTGCAT	CCTGATTCTC
	CCCACAGCTT	CAAGACCAAA	CTGGCCAAGG	ATATCTGTGC	CGACCCCAAG	AAGAAGTGGG	TGCAGGATTC
	CATGAAGTAT	CTGGACCAAA	AATCTCCAAC	TCCAAAGCCA	TAAATAATCA	CCATTTTTGA	AACCAAAACCA
50	GAGCCTGAGT	GTTGCCTAAT	TTGTTTTCCC	TTCTTACAAT	GCATTCTGAG	GTAACCTCAT	TATCAGTCCA
	AAGGGCATGG	GTTTTATTAT	ATATATATAT	ATATATTTTT	TTTTAAAAAA	AAACGTATTG	CATTTAATTT
	ATTGAGGCTT	TAAAACTTAT	CCTCCATGAA	TATCAGTTAT	TTTTAAACTG	TAAAGCTTTG	TGCAGATTCT
	TTACCCCTG	GGAGCCCCAA	TTGCATCCCC	TGTCACGTGT	GGGCAATGTT	CCCCCTCTCC	TCTCTTCTCT
	CCTGGAATCT	TGTAAAGGTC	CTGGCAAAGA	TGATCAGTAT	GAAAATGTCA	TTGTTCTTGT	GAACCCAAAG
55	TGTGACTCAT	TAAATGGAAG	TAATGTTGTT	TTAGGAATAC	ATAAAGTATG	TGCATATTTT	ATTATAGTCA
	CTAGTTGTAA	TTTTTTTGTG	GGAAATCCAC	ACTGAGCTGA	GGGGG-3'	(FRAG.NO:_)	(SEQ. ID
	NO: 2494)						
	5'-GCATTTTTC	AAGTTTATG	ATTTATTTAA	CTTGTGGAAC	AAAAATAAAC	CAGAAACCAC	CACCTCTCAC
	GCCAAAGCTC	ACACCTTCAG	CCTCCAACAT	GAAGGTCTCC	GCAGCACTTC	TGTGGCTGCT	GTCATAGCA
60	GCTGCCTTCA	GCCCCAGGG	GCTCGCTGGG	CCAGCTTCTG	TCCCAACCAC	CTGCTGCTTT	AACCTGGCCA

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ATAGGAAGAT ACCCCTTCAG CGACTAGAGA GCTACAGGAG AATCACCAGT GGCAAATGTC CCCAGAAAGC
 TGTGATCTTC AAGACCAAAC TGGCCAAGGA TATCTGTGCC GACCCCAAGA AGAAGTGGGT GCAGGATTCC
 ATGAAGTATC TGGACCAAAA ATCTCCAAC TCAAAGCCAT AAATAATCAC CATTTTGTAA ACCAAACCAG
 AGCCTGAGTG TTGCCTAATT TGTTTTCCCT TCTTACAATG CATCTGAGG TAACCTCATT ATCAGTCCAA
 5 AGGGCATGGG TTTTATTATA TATATATATA TTTTTTTTTT AAAAAAAAAA GTATTGCATT TAATTTATTG
 AGGCTTTAAA ACTTATCCTC CATGAATATC AGTTATTTTT AAAGTGTAAA GCTTTGTGCA GATTCTTTAC
 CCCCTGGGAG CCCCAATTG ATCCCCTGTC ACGTGTGGGC AATGTTCCCC CTCTCCTCTC TTCCTCCCTG
 GAATCTTGTA AAGGTCCTGG CAAAGATGAT CAGTATGAAA ATGTCAATGT TCTTGTGAAC CCAAAGTGTG
 ACTCATTAATA TGGAAAGTAAA TGTTGTTTTA GGAATAC-3' (FRAG.NO:_) (SEQ. ID NO:2491)
 10 5'-ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCCAG GGGCTCGCTG
 GGCCAGCTTC TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG ATACCCCTTC AGCGACTAGA
 GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA GCTGTGATCT TCAAGACCAA ACTGGCCAAG
 GATATCTGTG CCGACCCCAA GAAGAAAGTG GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA
 CTCCAAAGCC ATAA-3' (FRAG.NO:_) (SEQ. ID NO:2492)
 15 5'-CCACATATTC CCCTCCTTTT CCAAGGCAAG ATCCAGATGG ATTAAAAAAT GTACCAAGTC CCTCCTACTA
 GCTTGCTCTT CTCTGTCTT GCTTGACTTC CTAGGATCTG GAATCTGGTC AGCAATCAGG AATCCCTTCA
 TCGTGACCCC CGCATGGGCA AAGGCTTCCC TGGAAATCTCC CACACTGTCT GCTCCCTATA AAAGGCAGGC
 AGATGGGCCA GAGGAGCAGA GAGGCTGAGA CCAACCCAGA AACCACCACC TCTCAGCCA AAGCTCACAC
 CTTACGCCTC CAACATGAAG GTCTCCGAG CACTTCTGTG GCTGCTGCTC ATAGCAGCTG CCTTCAGCCC
 20 CCAGGGGCTC GCTGGGCCAG GTAAGCCCC CAACTCCTTA CAGGAAAGGT AAGGTAACCA CCTCCAGGCT
 ACTAGGTCAG CAAGAATCTT TACAGACTCA CTGCAAATTC TCCATTTGAA AAATAGGGAA ACAGGTTTTG
 TGGGTGGACA AGAAATGCCT CAACCGTCAC ATCCAGTCAC TGGAAGAGCC AGAACTAGAA AGCTCCCGAG
 TCTTTTCCCC ACATTCAAGA GGGCCGCTGG GTGCATCCTT ACCCAGCTAT CCTTACAGTG TTGGGAATG
 GGAATGGCT CTGTCTTACT GTGGGCATGG TGGGCATTTT TGGCAGTGGG AGAGAAGGAA AATCTGTTGA
 25 TTAGAAGCTC AGTATGTTAA TTCGACTCCA GGACAGCTTT CAGAGACAGT GGCTAAGAGA AGAAGCAGGT
 CCCAGGGGAT CTCTTGAGGT GACTTATTTT GACACTCTTT GGGAAAAGTTA TCTAGGAGAT TTGTTCCATA
 ACTCATTTTC CCATACTCTG GTGACAAATT TACTGAGTGT ATCGGTCCCA CTGAGCCAGT GCATAGCATG
 GTAACAAACA GTTCTAAATT ATCAATGACT TAACAGAATT AACTAAATTA ACAAAGTTA CTTTCTCACT
 TGTACTAAAT ATCTATAATG TATGGGCTCA GGCTTCTGCA TTTTATACTC AGGATTCTAG ACTGATGGAG
 30 AAGTTGCCAT GTGGGGGAAC ATTGATGGAT ACTGTGATAA AGCAGAAAGAA AGCTCTCAGG AGTCTTGCAT
 AGGCAATGCA CTGTGGCTCA AAAATGACAC CCATCACTTT GTCTCCTTCT TTATTGATCA AAATAATTA
 ATGCCTCCAA CCAAAACAAA GTGGCCAAAGA AATGCAAGTC TACCTTGTGT CTCAAAACAG AGGATGGAGA
 ATATTTGGTG AAAATTACCA TGACCATCAC ATGGCCACGT AGGTCTTTAT AATGACAGAG CTAGCATTTG
 TCACATTGAC CAAGCTTTGT CCATACACTC TACAGTAATG ATGAGTCCTC AGTGCACAGG GGAGGATGCT
 35 GAAGACACAG GACAGCATCC TCCAGACACA TAAGACTTCA GAGCAGAGGG ATTCTCCCTC CACCTCTCGC
 AATTCCTTGC TTTCTCCTAA CTTCCTTTAC AAAGTCATGC TTGGAAATGT CTATGTATCA TCATGTGGCT
 CATTTTTCCT TCTGTTCAAT TTTTTTCCCC AAAATTCAGC TTCTGTCCCA ACCACCTGCT GCTTTAACCT
 GGCCAATAGG AAGATACCCC TTCAGCGACT AGAGAGCTAC AGGAGAATCA CCAGTGGCAA ATGTCCCCAG
 AAAGCTGTGA TGTAAGTAAA TAAAGTTCAC CCTCCCCTAG ACAAAAAAAT AATGTCTAGG GCACAGAGTC
 40 AAGAAGTGTG GGAGTCATAG ACTCTGATAG TTTGACCTCT ATGGTCCAAT TCATTAATTT TCACAAAGTGA
 GTGTTCACTC CCAGCTCCCT GCCTGGGAGA TTGCTGTAGT CATATCAATT TCTTCAAGTC AAGAGCAAAAG
 ATGGTTTTAC TGGGCCTTTA AGAGCAGCAA CTAACCCAAAG AGTCTCATCC TTCCTCCTCT CCGTAGCAAC
 CCTTTGTCCA GGGGCAGATG GTCCCTTAAAT ATTTAGGGTC AAATGGGCAG AATTTTCAAA AACAATCCTT
 CCAATTGCAT CCTGATTCTC CCCACAGCTT CAAGACGAAA CTGGCCAAAG ATATCTGTGC CGACCCCAAG
 45 AAGAAGTGGG TGCAGGATTC CATGAAGTAT CTGGACCAAA AATCTCCAAC TCCAAAGCCA TAAATAATCA
 CCATTTTGA AACCAAAACCA GAGCCTGAGT GTTGCTTAAT TTGTTTTCCC TTCTTACAAT GCATTCTGAG
 GTAACCTCAT TATCAGTCCA AAGGGCATGG GTTTTATTAT ATATATATAT ATATATTTTT TTTTAAAAAA
 AAACGTATTG CATTTAATTT ATTGAGGCTT TAAAACTTAT CCTCCATGAA TATCAGTTAT TTTTAAACTG
 TAAAGCTTTG TGCAGATTCT TTACCCCTG GGAGCCCCAA TTCGATCCCC TGTCACGTGT GGGCAATGTT
 50 CCCCCTCTCC TCTCTTCTC CCTGGAATCT TGTAAGGTC CTGGCAAAGA TGATCAGTAT GAAAATGTCA
 TTGTTCTTGT GAACCCAAAG TGTGACTCAT TAAATGGAAG TAATGTTGTT TTAGGAATAC ATAAAGTATG
 TGCATATTTT ATTATAGTCA CTAGTTGTAA TTTTTTGTG GGAAATCCAC ACTGAGCTGA GGGGG-3' (FRAG.NO:_)
 (SEQ. ID NO:2493)

FK-506 Binding Protein Nucleic Acids and Oligonucleotide Fragments

55 5'- GCCAGGTGCG TGTTGGTCCA CGCCGCCCGT CGCGCCGCCC GCCCGCTCAG CGTCCGCCGC CGCCATGGGA
 GGCCGGAGCC GAGCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG GGCTGTGGG ACCGCTATGG
 GCGTGGAGAT CGAGACCATC TCCCCGGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAAA CGTGTGTGGT
 GCACTACACA GGAATGCTCC AAAATGGGAA GAAGTTTGAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG
 TTCAGAATTG GCAAAACAGGA AGTCATCAAA GGTTTTGAAG AGGGTGACG CCAGATGACG TTGGGGCAGA
 60 GGGCGAAGCT GACCTGCACC CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGTGTGTC TCCCTCCCAA
 TGCCACCCTC ATCTTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACTCA AGGTGGCTGG

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AGATGGCTGC TGCTCACCTT CCTAGCCTGC TCTGCCACTG GGACGGCTCC TGCTTTTGGG GCTCTTGATC
AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC TCTGCCCAAG TTGCTCTGTA TGTGTTTCGTC
AGTGTTCATG CGAATTCTTG CTTGAGGAAA CTTGCGTTGC AGATTGAAGC ATTTTCAGGTT GTGCATTTTG
TGTGATGCAT GTAGTAGCCT TTCCTGATGA CAGAACACAG ATCTCTTGTT CGCACAATCT AACTGTCCTT
5 ACCTTCACTT AAACCACACA CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA
CTTGAGCCAG TTACCTTTGC TGTCACCTTC TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC
CTCTTTGAGA AAATGTAAAA TAAAGGCTCT GTGCTTGACA GAATTCGGGC CGCCGCCAGG TCGCTGTTGG
TCCACGCCGC CCGTCGCGCC GCCCGCCCGC TCAGCGTCCG CCGCCGCCAT GGGAGTGCAG GTGGAAACCA
TCTCCCCAGG AGACGGGCGC ACCTTCCCCA AGCGCGGCCA GACCTGCGTG GTGCACTACA CCGGGATGCT
10 TGAAGATGGA AAGAAATTG ATTCTCCCG GGACAGAAAC AAGCCCTTTA AGTTTATGCT AGGCAAGCAG
GAGGTGATCC GAGGCTGGGA AGAAGGGGTT GCCCAGATGA GTGTGGGTCA GAGAGCCAAA CTGACTATAT
CTCCAGATTA TGCCTATGGT GCCACTGGGC ACCCAGGCAT CATCCACCA CATGCCACTC TCGTCTTCGA
TGTGGAGCTT CTAAACTGG AATGACAGGA ATGGCCTCCT CCCTTAGCTC CCGTCTCTTG GATCTGCCAT
GGAGGGATCT GGTGCCTCCA GACATGTGCA CATGAGTCCA TATGGAGCTT TTCCTGATGT TCCACTCCAC
15 TTTGTATAGA CATCTGCCCT GACTGAATGT GTTCTGTAC TCAGCTTTGC TTCCGACACC TCTGTTTCTT
CTTCCCCCTT CTCCTCGTAT GTGTGTTTAC CTAACATAA TGCCATAAAC TCCTCAAGTTA TCATTTTATT
TTGTTTTTAT TTTGGGGTGA AGATTCACTT TCAGTCTTTT GGATATAGGT TTCCAATTAA GTACATGGTC
AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG GAATTGGTGT TGGGGGGGGG GTTTGCAAGA
ATATTTTATT TTAATTTTTT GGATGAAATT TTTATCTATT ATATATTAAG CATTCTTGCT GCTGCGCTGC
20 AAAGCCATAG CAGATTTGAG GCGCTGTTGA GGACTGAATT ACTCTCCAAG TTGAGAGATG TCTTTGGGTT
AAATTAAGG CCCTACCTAA AACTGAGGTG GGGATGGGGA GAGCCTTTGC CTCCACCATT CCCACCCACC
CTCCCCTTAA ACCCTCTGCC TTTGAAAGTA GATCATGTTT ACTGCAATGC TGGACACTAC AGGTATCTGT
CCCTGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC TTTTTTTTTT TTCATCCTGT GGTTTTCTA
ATGGACTTTC AGGAATTTTG TAATCTCATA ACTTTCCAAG CTCCACCACT TCCTAAATCT TAAGAACITT
25 AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA CACCCAGTGA AAGCCAGCCT ATCATGACAA
ATCCTTGAGT GTTCTCTTAA GAAAATGATG TGTGTCATCG CAGCTTCAGC ATCTCCTGTT TTTTGATGCT
TGGCTCCCTC TGCTGATCTC AGTTTCTTGG CTTTCTCTCC CTCAGCCCTT TCTACCCCTT TTGCTGTCTT
GTGTAGTGAT TTGGTGAGAA ATCGTTGCTG CACCCCTCCC CCAGCACCAT TTATGAGTCT CAAGTTTTAT
TATTGCAATA AAAGTGCTTT ATGCCGAAT TC GCCGCCGCCA TGGGAGTGCA GGTGGAAACC ATCTCCCCAG
30 GAGACGGGCG CACCTTCCCC AAGCGCGGCC AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG
AAAGAAATTT GATTCTCCC GGGACAGAAA CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC
CGAGGCTGGG AAGAAGGGGT TGCCAGATG AGTGTGGGTC AGAGAGCCAA ACTGACTATA TCTCCAGATT
ATGCCTATGG TGCCACTGGG CACCCAGGCA TCATCCCACC ACATGCCACT CTCGTCTTCG ATGTGGAGCT
TCTAAACTG GAATGACAGG AATGGCCTCC TCCCTTAGCT CCCTGTCTT GGATCTGCCR TGGAGGGATC
35 TGGTGCTCC AGACATGTG ACATGARTCC ATATGGAGCT TTTCTGATG TTCCATCCCA CTTTGTATAG
ACATCTGCCC TGACTGAATG TGTCTGTCA CTCAGCTTTG CTTCCGACAC CTCTGTTTCC TCTTCCCCCT
TCTCTCGTA TGTGTGTTTA CTTAACTAT ATGCCATAA CCTCAAGTTA TTCA-3' (FRAG.NO:_) (SEQ. ID
NO:2499)
5'-GCCAGGTCGC TGTTGGTCCA CGCCGCCCGT CGCGCCGCCG GCCCGCTCAG CGTCCGCCGC CGCCATGGGA-3'
40 (FRAG. No:_) (SEQ. ID NO: 2495)
5'-GGCCGGAGCC GAGCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCGG GGCCTGTGGG CCGCTATGG
GCGTGGAGAT CGAGACCATC TCCCCGGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAAA CGTGTGTGGT
GCACTACACA GGAATGCTCC AAAATGGGAA GAAGTTTGAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG
TTCAGAATTG GCAGAACAGGA AGTCATCAAA GGTTTTGAAG AGGGTGAGC CCAGATGAGC TTGGGGCAGA
45 GGGCGAAGCT GACCTGCACC CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGGTGTCA TCCCTCCCAA
TGCCACCCTC ATCTTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACTCA AGGTGGCTGG
AGATGGCTGC TGCTCACCTT CCTAGCCTGC TCTGCCACTG GGACGGCTCC TGCTTTTGGG GCTCTTGATC
AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC TCTGCCCAAG TTGCTCTGTA TGTGTTTCGTC
AGTGTTCATG CGAATTCTTG CTTGAGGAAA CTTGCGTTGC AGATTGAAGC ATTTTCAGGTT GTGCATTTTG
50 TGTGATGCAT GTAGTAGCCT TTCCTGATGA CAGAACACAG ATCTCTTGTT CGCACAATCT AACTGCCTT
ACCTTCACTT AAACCACACA CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA
CTTGAGCCAG TTACCTTTGC TGTCACCTTC TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC
CTCTTTGAGA AAATGTAAAA TAAAGGCTCT GTGCTTGACA-3' (FRAG. NO:_) (SEQ. ID NO:2496)
5'-GAATTCGGGC CGCCGCCAGG TCGTGTGTTG TCCACGCCGC CCGTCGCGCC GCCCGCCCGC TCAGCGTCCG
55 CCGCCGCCAT GGGAGTGCA GGTGAAACCA TCTCCCCAGG AGACGGGCGC ACCTTCCCCA AGCGCGGCCA
GACCTGCGTG GTGCACTACA CCGGGATGCT TGAAGATGGA AAGAAATTTG ATCTCTCCCG GGACAGAAAC
AAGCCCTTTA AGTTTATGCT AGGCAAGCAG GAGGTGATCC GAGGCTGGGA AGAAGGGGTT GCCCAGATGA
GTGTGGGTCA GAGAGCCAAA CTGACTATAT CTCCAGATTA TGCTATGGT GCCACTGGGC ACCCAGGCAT
CATCCACCA CATGCCACTC TCGTCTTCGA TGTGGAGCTT CTAAACTGG AATGACAGGA ATGGCCTCCT
60 CCCTTAGCTC CCGTGTCTTG GATCTGCCAT GGAGGGATCT GGTGCCTCCA GACATGTGCA CATGATGCCA
TATGGAGCTT TTCCTGATGT TCCACTCCAC TTTGTATAGA CATCTGCCCT GACTGAATGT GTGTGTTTAC
TCAGCTTTGC TTCCGACACC TCTGTTTCTT CTTCCCTTTT CTCCTCGTAT GTGTGTTTAC CTAAACTATA

TGCCATAAAC CTCAAGTTAT TCATTTTATT TTGTTTTCAT TTTGGGGTGA AGATTCAGTT TCAGTCTTTT
 GGATATAGGT TTCCAATTAA GTACATGGTC AAGTATTAAC AGCACAAAGTG GTAGGTAAAC ATTAGAATAG
 GAATTGGTGT TGGGGGGGGG GTTTGCAAGA ATATTTTATT TTAATTTTTT GGATGAAATT TTTATCTATT
 ATATATTAAA CATCTTGCT GCTGCGCTGC AAAGCCATAG CAGATTTGAG GCGCTGTTGA GGACTGAATT
 5 ACTCTCCAAG TTGAGAGATG TCTTTGGGTT AAATTAAGG CCCTACCTAA AACTGAGGTG GGGATGGGGA
 GAGCCTTTGC CTCCACCATT CCCACCCACC CTCCCCTTAA ACCCTCTGCC TTTGAAAGTA GATCATGTTC
 ACTGCAATGC TGGACACTAC AGGTATCTGT CCTGGGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC
 TTTTTTTTTT TTCATCCTGT GGTTTTTCTA ATGGACTTTC AGGAATTTTG TAATCTCATA ACTTTCCAAG
 CTCCACCATT TCCTAAATCT TAAGAACCTT AATTGACAGT TTCAATTGAA GGTGCTGTTT GTAGACTTAA
 10 CACCCAGTGA AAGCCCAGCC ATCATGACAA ATCCTTGAAT GTTCTCTTAA GAAAATGATG CTGGTCATCG
 CAGCTTCAGC ATCTCCTGTT TTTTGATGCT TGGCTCCCTC TGCTGATCTC AGTTTCCTGG CTTTCCCTCC
 CTCAGCCCCT TCTACCCCT TTGCTGTCTT GTGTAGTGAT TTGGTGAGAA ATCGTGTCTG CACCCTTCCC
 CCAGCACCAT TTATGAGTCT CAAGTTTAT TATTGCAATA AAAGTGCTTT ATGCCCGAAT TC-3' (FRAG.NO:_)
 (SEQ. ID NO:2497)
 15 5' GCCGCCGCCA TGGGAGTGCA GGTGGAACC ATCTCCCCAG GAGACGGGCG CACCTTCCCC AAGCGCGGCC
 AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTT GATTCCTCCC GGGACAGAAA
 CAAGCCCTTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC CGAGGCTGGG AAGAAGGGGT TGCCCAGATG
 AGTGTGGGTC AGAGAGCCAA ACTGACTATA TCTCCAGATT ATGCCTATGG TGCCACTGGG CACCCAGGCA
 TCATCCCACC ACATGCCACT CTCGTCTTCG ATGTGGAGCT TCTAAACTG GAATGACAGG AATGGCCTCC
 20 TCCCTTAGCT CCCTGTTCTT GGATCTGCCR TGGAGGGATC TGGTGCCTCC AGACATGTGC ACATGARTCC
 ATATGGAGCT TTTCTGATG TTCCAATCCA CTTTGTATAG ACATCTGCCC TGAATGATG TGTTCTGTCA
 CTCAGCTTTG CTTCGACAC CTCTGTTTCC TCTCCCCTT TCTCCTCGTA TGTGTGTTTA CCTAACTAT
 ATGCCATAAA CCTCAAGTTA TTCA-3' (FRAG. NO:_) (SEQ. ID NO:2498)

wherein B is adenosine, or, more preferably, replaces adenosine and is an "equivale\lent" or a
 25 "universal" base, and adenosine A_{2a} receptor agonist or only minimally antagonist, an adenosine A_{2b}
 receptor antagonist, an adenosine A₃ receptor antagonist, or an adenosine A₁ receptor antagonist.
 Similarly, adenosine (A) may always be replaced by an "alternative", "equivalent" and/or "universal"
 base having a small fraction, preferably less than 0.3 of the activity of adenosine at the adenosine
 receptor(s), as described above.

30 In one preferred embodiment, the links between neighboring mononucleotides are phosphodiester
 links. In another preferred, at least one mononucleotide phosphodiester residue of the anti-sense
 oligonucleotide(s) is substituted by a methylphosphonate, phosphotriester, phosphorothioate,
 phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate,
 sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, 2'-O-methyl,
 35 methylene(methyimino), methyleneoxy (methylimino), phosphoramidate residues, and combinations
 thereof. The oligos having one or more phosphodiester residues substituted by one or more of the other
 residues are generally longer lasting, given that these residues are more resistant to hydrolysis than the
 phosphodiester residue. In some cases up to about 10%, about 30%, about 50%, about 75%, and even all
 phosphodiester residues may be substituted (100%). Typically, the multiple target anti-sense
 40 oligonucleotide (oligo) of the invention comprises at least about 7 mononucleotides, in some instances up
 to 60 and more mononucleotides, preferably about 10 to about 36, and more preferably about 12 to about
 21 mononucleotides. However, other lengths are also suitable depending on the length of the target
 macromolecule. Examples of the MTA oligos of the invention are provided in Table 3 below, which
 includes ninety-four sequences (SEQ ID NOS.: 2316 through 2410).

45 **Table 3: MTA Oligos, Location Targeted & Target**

MTA Oligo	SEQ. ID No.	Locati n	Compound Targeted	Target
<u>HUMNFKBP65A AS</u>				
CCC GGC CCC GCC TCG TGC C	3019	5' =1	EPI 2192	
50 CGT CCB TGC CGC GGG CCC	3020	5' =28 (AUG)	EPI 2193	

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	GGT CCC GCT TCT TC	3025	5'=362	EPI 2198
	GGG GTT GTT GTT GGT CTG G	3026	5'=401	EPI 2199
	TGT CCT CTT TCT GC	3026	5'=656	EPI 2200
	GCC TCG GGC CTC CC	3027	5'=697	EPI 2201
5	GGC TGG GGT CTG CGT	3028	5'=769	EPI 2202
	GGC CGG GGC TCG GTG GGT CCG CTG	3029	5'=953	EPI 2203
	GGG CTG GGG TGC TGG CTT GGG G	3030	5'=1022	EPI 2204
	GGG GCT GGG GCC TGG GCC	3031	5'=1208	EPI 2205
	GCC TGG GTG GGC TTG GGG GC	3032	5'=1272	EPI 2206
10	GCT GGG TCT GTG CTG TTG CC	3033	5'=1362	EPI 2207
	GTT GTG TGG GGG GCC	3034	5'=1451	EPI 2208
	GCT GGG TCG GGG GGC CTC TGG GCT GTC	3035	5'=1511	EPI 2209
	GCC CCG GGG CCC CC	3036	5'=1550	EPI 2210
	TGG CTC CCC CCT CC	3037	5'=1772	EPI 2211
15	GCT CCC CCC TTT CC	3038	5'=1863	EPI 2212
	CGG ACG AAG ACA GAG A	3039	5'=1979	EPI 2213
	GGC TTT GTG GGC TC	3040	5'=2011	EPI 2214
	GCC TGC TCT CCC CC	3041	5'=2312	EPI 2215
	CCC GGC CCC GCC BCG BBC C	3042	intron	EPI 2192-01A HSU50136C4Synth
20	CCC GGC CCC GCC BCG	3043	intron	EPI 2192-01B
	CCC GGC CCC GCC BCG BBC C	3044	5'untr	EPI 2192-02A HUMLIPOX5LO
	CCC GGC CCC GCC BCG	3045	5'untr	EPI 2192-02B
	CCC GBC CCC GCC TCB BG	3046	trans	EPI 2192-03A HSNFKBS Subunit
	CCC GBC CCC GCC TC	3047	trans	EPI 2192-03B
25	CCG GCC CCG CCT C	3048	5'untr	EPI 2192-04 TGFβR1
	CCC GBB CCC GCB TBG TGC C	3049	5'trans	EPI 2192-05A HSU58198I1 enhan
	CCC GCB TBG TGC C	3050	5'untr	EPI 2192-05B
	CCC GGB CCC BCC BBG TGC C	3051	3'trans	EPI 2192-06 HSVECAD
	CBG BBC CCG CCT CGT GCC	3052	intron	EPI 2192-07A NFKB2
30	C CCG CCT CGT GCC	3053	intron	EPI 2192-07B NFKB2
	CCG GCB CCG CCT CBT GCC	3054	5'trans	EPI 2192-08 Carboxypep
	CCG GCC CCG CCB CBT GCC	3055	3'trans	EPI 2192-09 HumADRA2Ca2AdrKid
	CCC GBC CCC GBC TCG	3056	5'untrs	EPI 2192-10 HUMFK506B
	CCC GGC CBC GBC TCG	3057	5'untrs	EPI 2192-11 HSNBARKS1βAdrKin
35	CCC GGC CCB GCC TBG	3058	5'UTR	EPI 2192-12 HSNFXN1 (NFKB1)
	CCC GGC BCB GBC TCG TBC C	3059	3'UTR	EPI 2192-13 HSILF(transcrp. Factor ILF)
	CCC GGC CCC GCC BCG	3060		EPI-2192-14 NFKB/C4Syn/5-LO/ TGFBrecl MTA
40	CCC GGC CCC GCC BCG	3061		EPI-2192-15NFKB/C4Syn/5-LOMTA
	TCC BTG CCG CGG GC	3062	3' trans	EPI-2193-01 METOncogene
	TCC BTG CCB CGG GCC	3063	3' trans	EPI-2193-02 HSFRG2 (IG)
	TCC BTG CCB CGG GCC	3064	mid cod	EPI-2193-03 5-LO
	TCC BTG CCB CBG GCC	3065	mid cod	EPI-2193-04 HUMTK14
45	GTC CBT GBC GCG G	3066	3'trans	EPI-2193-05 HUMTNFR
	TC CBT GBC GCG GG	3067	AUG	Probl.HUMPTCH cardiacK+channel
	TCT GBG CTC CTC TBB CCT GGG	3068	intr	EPI-2195-01 humCSPAcytotox. Ser.Protease
50	CTG TGC BCC TBB CBC CTG GG	3069	intr	EPI-2195-02 HSINOSX08induc.NOS
	TGT GBT CCB CTB GBC TGG G	3070		EPI-2195-03 HUMACHRM2muscl.m2 acetylch.rec.
	TCT GTB CTC BBC TCB CCT G	3071		EPI-2195-04 s86371sl Neurokinin3Recept
55	TGC TCC TCB CBB CTG GG	3072		EPI-2195-05 HUMMIP1 Amacro
	inflam.factor			

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Table 3: MTA Oligos, Location Targeted & Target (Cont'd)

MTA Oligo	SEQ. ID No.	L cati n	Compound Targeted	Target
5 CTC CTC TBG CCT GG	3073		EPI-2195-06	HSNBARKS4 β-Adr Rec Kinase
GTG CTC CBB TCB BCT GGG	3074		EPI-2195-07	HSTNFR2SO6TNF R2
GTG CBC CBB TCB CCT GGG	3075		EPI-2195-08	humfkbk fk506 binding prot.
10 TCT GTG CBC CTC TBG BCT	3076	exon	EPI-2195-09	HSNBARKS1β-Adr. Recept. Kinase
CTG TBB TCC TBB CBC CTG G	3077	intron	EPI-2195-10	HUMIL8
TGT GCT BBT CBC BCB TGG G	3078		EPI-2195-11	HSU50157 PDE4
GTG CBC CBC TCB CCT G	3079	intron/exon	EPI-2195-12	IL-2 R
CTG TGC BCC TCT C	3080	3'UTR	EPI-2203-05	IL-6 R HSIL6R
15 CBG TGC BCC BCT CBC CTG	3081	intr/ex	EPI-2203-06A	HSIL2rG6
G TGC BCC BCT CBC CTG	3082	intr/ex	EPI-2203-06B	HSIL2rG6
CBC CTC TCB CCT GGG	3083	coding	EPI-2203-07A	HUMIL71
C CTC TCB CCT GGG	3084	coding	EPI-2203-07B	IL-7 HUMIL71
GCT CCB CTC GCT T	3085	coding	EPI-2203-08	IL-6 R HSI6REC
20 TGC TCC TCB CGC C	3086	intron PDGF A	EPI-2303-09	Chain HUMPDGFAB
GTT GTT GBT CTG G	3087	3'utr	EPI-2199-01	GATA-4Transcrip. Factor for IL-5
GGT TGB BBT TGG TCT TGG	3088	Coding	EPI-2199-02	TNFα HUMTNFA
GGT TGT TGB TGB TCT G	3089	Far 5'UTR	EPI-2199-03	HSSUBP1G(Sub Pr)
25 GGG TTB BBG TTG BTC TGG	3090	Coding	EPI-2199-04	NeutrophilAdh. R HUMNARIA
GGG TTB BBG TTG BTC TGG	3091	HSHM2	EPI-2199-05	m2 Muscarinic R
TTG TTG TBG BTC TGG	3092	HUML1CAM	EPI-2199-06	L1 LeukAadhProt
GGG TBG BBG BGT CCG CTG	3093	coding	EPI-2203-01	HUMGATA2A
30 GGG TCB GBG GBT CBG CTG	3094	S71424S2	EPI-2203-02	IGE eps
GGG TBG GTG GGT C	3095	coding	EPI-2203-03	HSGCSFR2
GGG TCG GBG GGT CBG C	3096	HUMITGF	EPI-2203-04	TGFβ3
GGG TGG GCT T	3097	HUMNK65PRO	EPI-2206-01	NFKB/NK & TCell Activating Prot
35 GGG TGG GCT TGG G	3098	HUMPEREEB	EPI 2206-02	NFKB/Prostagl. EP3 Rec
CCTGGGTGGGBBTGGG	3099		EPI 2206-03	HSNF2B/GCSF NFKB/GranuLocCSF/ Transcr. FactorNF2B
40 CCTGGBTGGGCBTGGG	3100		EPI-2206-04	HUMLAP/NFKB Leuk. Adhes. Prot
GCCTGBGTGBBCTTGGG	3101		EPI2206-05	NFKB/Endothel N2 S63833
45 CCCAVGVCCVCCCAGGC	3102		EPI 2206-06	NFKBAS13/B Lymph SerThrProt. Kinase
AGCCCCACCCAGGC	3103		EPI2206-07	NFKBAS13/GCSF1 HSGCSFR1Rec
50 BCCTGGGTGGGCTB	3104		EPI2206-08	NFKBAS13/GCSF1/ NK7TCELLACT. Prot
GGTGGGCTTGGG	3105		EPI 2206-09	NFKBAS13/ HSTGFB1 TGFB
CCBBGGTGGGCTTGGG	3106		EPI 2206-10	NFKBAS13/ HSTGFB1 TGFB1
55 CTGGGTGGGBBTGGG	3107		EPI 2206-11	NFKBAS13/ HSGCSFR1 GCSFR1
CCBGGGTGGGCTTGG	3108		EPI 2206-12	NFKBAS13/HUMCD30A LymphActAntigCoding
GGGTGGGCTTGG	3109		EPI-2206-12B	NFKBAS13/HUMCD30A
60 CCTGBGTGBGCBTGGG	3110		EPI 2206-13	NFKBAS13/HUMCAM1V Vasc. Endoth. Cell Adh. Molec

B: Universal Base

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The MTA oligos of Table 3 are suitable for use with two or more of the targets listed in Table 4 below.

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Table 4: Targets for the MTA Oligos of Table 3

Compound	Target
EPI 2010	Adenosine A1 receptor
EPI 2045	Adenosine A3 receptor
EPI 2873, EPI 2193	NFκB
EPI 1873	Interleukin-1
EPI 1857	Interleukin -5
EPI 2945	Interleukin -4
EPI 2977	Interleukin -8
EPI 2031	5-Lipoxygenase
EPI 1898	Leukotriene C-4 Synthase
EPI 1856	Eotaxin
EPI 1131	ICAM
EPI 1085	VCAM
EPI 2085	TNFα
EPI 1908	PAF
EPI 1925	IL-4 receptor
EPI 2643	β2 adrenergic receptor kinase
EPI 2934	Tryptase
EPI 2033	Major Basic Protein
EPI 2795	Eosinophil Peroxidase

NfκB: nuclear factor κB

ICAM: intracellular adhesion molecule

VCAM: vascular cell adhesion molecule

TNF: tumor necrosis factor

PAF: platelet activating factor

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The mRNA sequence of the targeted protein may be derived from the nucleotide sequence of the gene expressing the protein, whether for existing targets or those to be found in the future. Sequences for many target genes of different systems are presently known. See, GenBank data base, NIH, the entire sequences of which are incorporated here by reference. The sequences of those genes, whose sequences are not yet available, may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, anti-sense oligonucleotides are produced as described above and utilized to validate the target by in vivo administration and testing for a reduction of the production of the targeted protein in accordance with standard techniques, and of specific functions. As already described above, the anti-sense oligonucleotides may be of any suitable length, e.g., from about 7 to about 60 nucleotides in length, depending on the particular target being bound and the mode of delivery thereof. The anti-sense oligonucleotide preferably is directed to an mRNA region containing a junction between intron and exon or to regions vicinal to the junction. Where the anti-sense oligonucleotide is directed to an intron/exon junction, it may either entirely overlie the junction or may be sufficiently close to the junction to inhibit splicing out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g., with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, 10, 5, 3, or 2 nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon and, more generally, those that target the coding region of the target mRNA. When practicing the present invention, the anti-sense oligonucleotides administered may be related in origin to the species to which it is administered. When treating humans, human anti-sense may be used if desired. Anti-sense oligos to endogenous sequences from other species,

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however, are also encompassed.

Pharmaceutical compositions comprising an anti-sense oligonucleotide as given above effective to reduce expression of an A₁ or A₃ adenosine receptor by passing through a cell membrane and binding specifically with mRNA encoding an A₁ or A₃ adenosine receptor in the cell so as to prevent its translation are another aspect of the present invention. Such compositions are provided in a suitable pharmaceutically acceptable carrier, e.g., sterile pyrogen-free saline solution. The anti-sense oligonucleotides may be formulated with a hydrophobic carrier capable of passing through a cell membrane, e.g., in a liposome, with the liposomes carried in a pharmaceutically acceptable aqueous carrier. The oligonucleotides may also be coupled to a substance which inactivates mRNA, such as a ribozyme. Such oligonucleotides may be administered to a subject to inhibit the activation of a target, such as the adenosine receptors, which subject is in need of such treatment for any of the reasons discussed herein. Furthermore, the pharmaceutical formulation may also contain chimeric molecules comprising anti-sense oligonucleotides attached to molecules which are known to be internalized by cells. These oligonucleotide conjugates utilize cellular uptake pathways to increase cellular concentrations of oligonucleotides. Examples of macromolecules used in this manner include transferrin, asialoglycoprotein (bound to oligonucleotides via polylysine) and streptavidin. In the pharmaceutical formulation, the anti-sense compound may be contained within a lipid particle or vesicle, such as a liposome or microcrystal. The particles may be of any suitable structure, such as unilamellar or plurilamellar, so long as the anti-sense oligonucleotide is contained therein. Positively charged lipids such as N- [1-(2, 3 -dioleoyloxy) propyl] -N, N, N-trimethylammoniumethylsulfate, or "DOTAP," are particularly preferred for such particles and vesicles. The preparation of such lipid particles is well known. See, e.g., U.S. Patent Nos. 4,880,635 to Janoff et al.; 4,906,477 to Kurono et al.; 4,911,928 to Wallach; 4,917,951 to Wallach; 4,920,016 to Allen et al.; 4,921,757 to Wheatley et al.; etc.

Subjects may be administered the active composition by any means which transports the anti-sense nucleotide composition to the lung. The anti-sense compounds are particularly disclosed herein may be administered to the lungs of a patient by any suitable means, but are preferably administered by generating an aerosol comprised of respirable particles, the respirable particles comprised of the anti-sense compound, which particles the subject inhales. The respirable particles may be liquid or solid. The particles may optionally contain other therapeutic ingredients. Particles comprised of anti-sense compound for practicing the present invention should include particles of respirable size: that is, particles of a size sufficiently small to pass through the mouth and larynx upon inhalation and into the bronchi and alveoli of the lungs. In general, particles ranging from about .5 to about 10 microns in size are respirable. Particles of non-respirable size which are included in the aerosol tend to deposit in the throat and be swallowed, and the quantity of non-respirable particles in the aerosol is preferably minimized. For nasal administration, a particle size in the range of 10-500 :m is preferred to ensure retention in the nasal cavity. Thus, particles of about 4, about 10, about 25, about 50 to about 75, about 100, about 250, about 500, and other specific ranges therewithin, are preferred. Others, however, are also contemplated within the confines of this invention.

Liquid pharmaceutical compositions of active compound for producing an aerosol can be prepared by combining the anti-sense compound with a suitable vehicle, such as sterile pyrogen free water. Other therapeutic compounds may optionally be included. Solid particulate compositions containing respirable dry particles of micronized anti-sense compound may be prepared by grinding dry anti-sense compound with a mortar and pestle, and then passing the micronized composition through a 400 mesh screen to break up or separate out large agglomerates. A solid particulate composition comprised of the anti-sense compound may optionally contain a dispersant which serves to facilitate the formation of an aerosol. A suitable dispersant is lactose, which may be blended with the anti-sense compound in any suitable ratio (e.g., a 1 to 1 ratio by weight). Again, other therapeutic compounds may also be included.

The dosage of the anti-sense compound administered will depend upon the disease being treated, the condition of the subject, the particular formulation, the route of administration, the timing of administration to a subject, etc. In general, intracellular concentrations of the oligonucleotide of from about

0.01, about 0.05, about 0.1, about 0.2, about 1 to about 5 μ M, about 50 μ M, about 100 μ M or more, and more particularly about 0.2 to about 0.5 μ M, are desired. For administration to a subject such as a human, a dosage of from about 0.01, about 0.1 or about 1 mg/Kg up to about 50, about 100, or about 150 mg/Kg and even higher doses are typically employed depending on the route of administration as is known in the art.

- 5 Depending on the solubility of the particular formulation of active compound administered, the daily dose may be divided among one or several unit dose administrations. Administration of the anti-sense compounds may be carried out therapeutically (i.e., as a rescue treatment) or prophylactically. Aerosols of liquid particles comprising the anti-sense compound may be produced by any suitable means, such as with a nebulizer. See, e.g., U.S. Patent No. 4,501,729. Nebulizers are commercially available devices which
- 10 transform solutions or suspensions of the active ingredient into a therapeutic aerosol mist either by means of acceleration of a compressed gas, typically air or oxygen, through a narrow venturi orifice or by means of ultrasonic agitation. Suitable formulations for use in nebulizers consist of the active ingredient in a liquid carrier, the active ingredient comprising up to 40% w/w of the formulation, but preferably less than 20% w/w. The carrier is typically water or a dilute aqueous alcoholic solution, preferably made isotonic
- 15 with body fluids by the addition of, for example, sodium chloride. Optional additives include preservatives if the formulation is not prepared sterile, for example, methyl hydroxybenzoate, antioxidants, flavoring agents, volatile oils, buffering agents and surfactants.

- In one preferred embodiment, the pharmaceutical composition comprises nucleic acid(s) which comprise the anti-sense oligo(s) described above and one or more surfactants. Suitable surfactants or
- 20 surfactant components for enhancing the uptake of the anti-sense oligonucleotides of the invention include synthetic and natural as well as full and truncated forms of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant Protein E, di-saturated phosphatidylcholine (other than dipalmitoyl), dipalmitoylphosphatidylcholine, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine; phosphatidic acid, ubiquinones,
- 25 lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycerol-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate; as well as natural and artificial lamellar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid,
- 30 polyenoic acid, lecithin, palmitic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly (vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. These surfactants may be used either as a single, or as part of a multiple component, surfactant in a formulation, or as covalently bound additions to the 5' and/or
- 35 3' ends of the anti-sense oligo(s). Aerosols of solid particles comprising the active compound may likewise be produced with any solid particulate medicament aerosol generator. Aerosol generators for administering solid particulate medicaments to a subject produce particles which are respirable, as explained above, and generate a volume of aerosol containing a predetermined metered dose of a medicament at a rate suitable for human administration. One illustrative type of solid particulate aerosol
- 40 generator is an insufflator. Suitable formulations for administration by insufflation include finely comminuted powders which may be delivered by means of an insufflator or taken into the nasal cavity in the manner of a snuff. In the insufflator, the powder (e.g., a metered dose thereof effective to carry out the treatments described herein) is contained in capsules or cartridges, typically made of gelatin or plastic, which are either pierced or opened in situ and the powder delivered by air drawn through the device upon
- 45 inhalation or by means of a manually-operated pump. The powder employed in the insufflator consists either solely of the active ingredient or of a powder blend comprising the active ingredient, a suitable powder diluent, such as lactose, and an optional surfactant. The active ingredient typically comprises from 0.1 to 100 w/w of the formulation. A second type of illustrative aerosol generator comprises a metered dose inhaler. Metered dose inhalers are pressurized aerosol dispensers, typically containing a suspension or

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solution formulation of the active ingredient in a liquefied propellant. During use these devices discharge the formulation through a valve adapted to deliver a metered volume, typically from 10 to 150 :l, to produce a fine particle spray containing the active ingredient. Suitable propellants include certain chlorofluorocarbon compounds, for example, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane and mixtures thereof. The formulation may additionally contain one or more co-solvents, for example, ethanol, surfactants, such as oleic acid or sorbitan trioleate, antioxidants and suitable flavoring agents. The aerosol, whether formed from solid or liquid particles, may be produced by the aerosol generator for example at a rate of from about 10, about 30, about 70 to about 100, about 150, about 150 liters per minute, more preferably from about 30 to 150 liters per minute, and most preferably about 60 liters per minute. Aerosols containing greater amounts of medicament, however, may be administered more rapidly as is known in the art.

The relevant disclosures of all scientific publications and patent references cited in this patent are specifically intended to be incorporated herein by reference, particularly in reference to preparatory methods and technologies which are enabling of the invention. The following examples are provided to illustrate the present invention, and should not be construed as limiting thereon.

EXAMPLES

In the following examples, :M means micromolar, ml means milliliters, :m means micrometers, mm means millimeters, cm means centimeters, EC means degrees Celsius, :g means micrograms, mg means milligrams, g means grams, kg means kilograms, M means molar, and h or hr. means hours.

20 Example 1: Design and Synthesis of Anti-sense Oligonucleotides

The design of anti-sense oligonucleotides against the A₁ and A₃ adenosine receptors may require the solution of the complex secondary structure of the target A₁ receptor mRNA and the target A₃ receptor mRNA. After generating this structure, anti-sense nucleotide are designed which target regions of mRNA which might be construed to confer functional activity or stability to the mRNA and which optimally may overlap the initiation codon. Other target sites are readily usable. As a demonstration of specificity of the anti-sense effect, other oligonucleotides not totally complementary to the target mRNA, but containing identical nucleotide compositions on a w/w basis, are included as controls in anti-sense experiments.

The mRNA secondary structure of the adenosine A₁ receptor was analyzed and used as described above. to design a phosphorothioate anti-sense oligonucleotide. The anti-sense oligonucleotide which was synthesized was designated HAdA₁AS and had the following sequence: 5' -GAT GGA GGG CGG CAT GGC GGG-3' (SEQ ID NO:1). As a control, a mismatched phosphorothioate anti-sense nucleotide designated HAdAIMM1 was synthesized with the following sequence: 5' -GTA GCA GGC GGG GAT GGG GGC-3' (SEQ ID NO:2). Each oligonucleotide had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligonucleotide was specific for the human and rabbit adenosine A₁ receptor genes, and that the mismatched control was not a candidate for hybridization with any known gene sequence.

The secondary structure of the adenosine A₃ receptor mRNA was similarly analyzed and used as described above to design two phosphorothioate anti-sense oligonucleotides. The first anti-sense oligonucleotide (HAdA₃AS1) synthesized had the following sequence: 5' -GTT GTT GGG CAT CTT GCC-3' (SEQ ID NO:3). As a control, a mismatched phosphorothioate anti-sense oligonucleotide (HAdA₃MM1) was synthesized, having the following sequence: 5' -GTA CTT GCG GAT CTA GGC-3' (SEQ ID NO:4). A second phosphorothioate anti-sense oligonucleotide (HAdA₃AS2) was also designed and synthesized, having the following sequence: 5' -GTG GGC CTA GCT CTC GCC-3' (SEQ ID NO:5). Its control oligonucleotide (HAdA₃MM2) had the sequence: 5' -GTC GGG GTA CCT GTC

Receptor Anti-sense Oligos

The anti-sense oligonucleotide against the human A₁ receptor (SEQ ID NO:1) described above, was tested for efficacy in an in vitro model utilizing lung adenocarcinoma cells HTB-54. HTB-54 lung adenocarcinoma cells were demonstrated to express the A₁ adenosine receptor using standard northern blotting procedures and receptor probes designed and synthesized in the laboratory.

HTB-54 human lung adenocarcinoma cells (106/100 mm tissue culture dish) were exposed to 5.0 :M HAdAlAS or HAdAIMM1 for 24 hours, with a fresh change of media and oligonucleotides after 12 hours of incubation. Following 24 hour exposure to the oligonucleotides, cells were harvested and their RNA extracted by standard procedures. A 21-mer probe corresponding to the region of mRNA targeted by the anti-sense (and therefore having the same sequence as the anti-sense, but not phosphorothioated) was synthesized and used to probe northern blots of RNA prepared from HAdAlAS-treated, HAdAIMM1-treated and non-treated HTB-54 cells. These blots showed clearly that HAdAlAS but not HAdAIMM1 effectively reduced human adenosine receptor mRNA by >50%. This result showed that HAdAlAS is a good candidate for an anti-asthma drug since it depletes intracellular mRNA for the adenosine A₁ receptor, which is involved in asthma.

Example 3: In Vivo Efficacy of Adenosine A₁ Receptor Anti-sense Oligos

A fortuitous homology between the rabbit and human DNA sequences within the adenosine A₁ gene overlapping the initiation codon permitted the use of the phosphorothioate anti-sense oligonucleotides initially designed for use against the human adenosine A₁ receptor in a rabbit model. Neonatal New Zealand white Pasteurella-free rabbits were immunized intraperitoneally within 24 hours of birth with 312 antigen units/ml house dustmite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA), mixed with 10% kaolin. Immunizations were repeated weekly for the first month and then biweekly for the next 2 months. At 3-4 months of age, eight sensitized rabbits were anesthetized and relaxed with a mixture of ketamine hydrochloride (44 mg/kg) and acepromazine maleate (0.4 mg/kg) administered intramuscularly. The rabbits were then laid supine in a comfortable position on a small molded, padded animal board and intubated with a 4.0-mm intratracheal tube (Mallinkrodt, Inc., Glens Falls, NY). A polyethylene catheter of external diameter 2.4 mm with an attached latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiments. The intratracheal tube was attached to a heated Fleisch pneumotachograph (size 00; DOM Medical, Richmond, VA), and flow was measured using a Validyne differential pressure transducer (Model DP-45161927; Validyne Engineering Corp., Northridge, CA) driven by a Gould carrier amplifier (Model 11-4113; Gould Electronic, Cleveland, OH). The esophageal balloon was attached to one side of the differential pressure transducer, and the outflow of the intratracheal tube was connected to the opposite side of the pressure transducer to allow recording of transpulmonary pressure. Flow was integrated to give a continuous tidal volume, and measurements of total lung resistance (RL) and dynamic compliance (C_{dyn}) were calculated at isovolumetric and flow zero points, respectively, using an automated respiratory analyzer (Model 6; Buxco, Sharon, CT). Animals were randomized and on Day 1 pretreatment values for PC50 were obtained for aerosolized adenosine. Anti-sense (HAdAlAS) or mismatched control (HAdAIMM) oligonucleotides were dissolved in sterile physiological saline at a concentration of 5000 :g (5 mg) per 1.0 ml. Animals were subsequently administered the aerosolized anti-sense or mismatch oligonucleotide via the intratracheal tube (approximately 5000 :g in a volume of 1.0 ml), twice daily for two days. Aerosols of either saline, adenosine, or anti-sense or mismatch oligonucleotides were generated by an ultrasonic nebulizer (DeVilbiss, Somerset, PA), producing aerosol droplets 80% of which were smaller than 5 :m in diameter. In the first arm of the experiment, four randomly selected allergic rabbits were administered anti-sense oligonucleotide and four the mismatched control oligonucleotide. On the morning of the third day, PC50 values (the concentration of aerosolized adenosine in mg/ml required to reduce the dynamic compliance of the bronchial airway 50% from the baseline value) were obtained and compared to PC50 values obtained for these animals prior to exposure to oligonucleotide. Following a 1 week interval, animals were crossed

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over, with those previously administered mismatch control oligonucleotide now administered anti-sense oligonucleotide, and those previously treated with anti-sense oligonucleotide now administered mismatch control oligonucleotide. Treatment methods and measurements were identical to those employed in the first arm of the experiment. It should be noted that in six of the eight animals treated with anti-sense oligonucleotide, adenosine-mediated bronchoconstriction could not be obtained up to the limit of solubility of adenosine, 20 mg/ml. For the purpose of calculation, PC50 values for these animals were set at 20 mg/ml. The values given therefore represent a minimum figure for anti-sense effectiveness. Actual effectiveness was higher. The results of this experiment are illustrated in Table 5 below.

Table 5: Effect of Adenosine A₁ Receptor Anti-sense Oligo upon PC50 Values in Asthmatic Rabbits

Mismatch Control		A ₁ Receptor Anti-sense Oligo	
Pre Oligonucleotide	Post Oligonucleotide	Pre Oligonucleotide	Post Oligonucleotide
3.56 ± 1.02	5.16 ± 1.03	2.36 ± 0.68	>19.5 ± 0.34**

The results are presented as the mean (n=8) ± SEM.

The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test.

**Significantly different from all other groups, p<0.01.

In both arms of the experiment, animals receiving the anti-sense oligonucleotide showed an order of magnitude increase in the dose of aerosolized adenosine required to reduce dynamic compliance of the lung by 50%. No effect of the mismatched control oligonucleotide upon PC50 values was observed. No toxicity was observed in any animal receiving either anti-sense or control inhaled oligonucleotide. These results show clearly that the lung has exceptional potential as a target for anti-sense oligonucleotide-based therapeutic intervention in lung disease. They further show, in a model system which closely resembles human asthma, that downregulation of the adenosine A₁ receptor largely eliminates adenosine-mediated bronchoconstriction in asthmatic airways. Bronchial hyperresponsiveness in the allergic rabbit model of human asthma is an excellent endpoint for anti-sense intervention since the tissues involved in this response lie near to the point of contact with aerosolized oligonucleotides, and the model closely simulates an important human disease.

Example 4: Specificity of A₁-adenosine Receptor Anti-sense Oligonucleotide

At the conclusion of the cross-over experiment of Example 3 above, airway smooth muscle from all rabbits was quantitatively analyzed for adenosine A₁ receptor number. As a control for the specificity of the anti-sense oligonucleotide, adenosine A₂ receptors, which should not have been affected, were also quantified. Airway smooth muscle tissue was dissected from each rabbit and a membrane fraction prepared according to the method of Kleinstein et al. (Kleinstein, J. and Glossmann, H., Naunyn-Schmiedeberg's Arch. Pharmacol. 305: 191-200 (1978)), the relevant portion of which is hereby incorporated in its entirety by reference, with slight modifications. Crude plasma membrane preparations were stored at 70EC until the time of assay. Protein content was determined by the method of Bradford (M. Bradford, Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference). Frozen plasma membranes were thawed at room temperature and were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37EC to remove endogenous adenosine. The binding of [³H] DPCPX (A₁ receptor-specific) or [³H] CGS-21680 (A₁ receptor-specific) was measured as previously described by Ali et al. (Ali, S. et al., J. Pharmacol. Exp. Ther. 268, Am. J. Physiol 266, L271-277 (1994), the relevant portion of which is hereby incorporated in its entirety by reference). The animals treated with adenosine A₁ anti-sense oligonucleotide in the cross-over experiment had a nearly 75% decrease in A₁ receptor number compared to controls, as assayed by specific binding of the A₁-specific antagonist DPCPX. There was no change in adenosine A₂ receptor number, as assayed by specific binding of the A₂ receptor-specific agonist 2- [p- (2-carboxyethyl)-phenethylamino] -5' - (N-ethylcarboxamido) adenosine (CGS-21680). This is illustrated in Table 6 below.

Table 6: Specificity of Action of Adenosine A₁ Receptor Oligonucleotide Anti-sense

A₁-Specific Binding	1105 ± 48**	293 ± 18
A₂-Specific Binding	302 ± 22	442 ± 171

The results are presented as the mean (n = 8) ± SEM.

The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test.

**Significantly different from mismatch control, p<0.01.

- 5 The above results illustrate the effectiveness of anti-sense oligonucleotides in treating airway disease. Since the anti-sense oligos described above, eliminate the receptor systems responsible for adenosine-mediated bronchoconstriction, it may be less imperative to eliminate adenosine from them. However, it would be preferable to eliminate adenosine from even these oligonucleotides to reduce the dose needed to attain a similar effect. Described above are other anti-sense oligonucleotides targeting mRNA of proteins involved in inflammation. Adenosine has been eliminated from their nucleotide content to prevent its liberation during degradation.

Example 5: Anti-sense Oligos directed to other Target Nucleic Acids

- 15 This work was conducted to demonstrate that the present invention is broadly applicable to anti-sense oligonucleotides ("oligos") specific to nucleic acid targets broadly. The following experimental studies were conducted to show that the method of the invention is broadly suitable for use with anti-sense oligos designed as taught by this application and targeted to any and all adenosine receptor mRNAs. For this purpose, various anti-sense oligos were prepared to adenosine receptor mRNAs exemplified by the adenosine A₁, A_{2b} and A₃ receptor mRNAs. Anti-sense Oligo I was disclosed above (SEQ. ID NO:1). Five additional anti-sense phosphorothioate oligos were designed and synthesized as indicated above.

- 20 1- Oligo II (SEQ. ID NO: 7) also targeted to the adenosine A₁ receptor, but to a different region than Oligo I.
2- Oligo V (SEQ. ID NO: 10) targeted to the adenosine A_{2b} receptor.
3- Oligos III (SEQ. ID NO: 8) and IV (SEQ. ID NO: 9) targeted to different regions of the adenosine A₃ receptor.
4- Oligo I-PD (SEQ. ID NO: 1681) (a phosphodiester oligo of the same sequence as Oligo I).

- 25 These anti-sense oligos were designed for therapy on a selected species as described above and are generally specific for that species, unless the segment of the target mRNA of other species happens to contain a similar sequences. All anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application.

Example 6: Design & Sequences of other Anti-sense Oligos

- 30 Six oligos and their effects in a rabbit model were studied and the results of these studies are reported and discussed below. Five of these oligos were selected for this study to complement the data on Oligo I (SEQ ID NO: 1) provided in Examples 1 to 4 above. This oligo is anti-sense to one region of the adenosine A₁ receptor mRNA. The oligos tested are identified as anti-sense Oligos I (SEQ ID NO: 1) and II (SEQ. ID No: 7) targeted to a different region of the adenosine A₁ receptor mRNA, Oligo V (SEQ. ID No:8) targeted to the adenosine A_{2b} receptor mRNA, and anti-sense Oligos III and IV (SEQ. ID NOS: 9 and 10) targeted to two different regions of the adenosine A₃ receptor mRNA. The sixth oligo (Oligo I-PD) is a phosphodiester version of Oligo I (SEQ. ID NO:1). The design and synthesis of these anti-sense oligos was performed in accordance with Example 1 above.

(I) Anti-sense Oligo I

- 40 The anti-sense oligonucleotide I referred to in Examples 1 to 4 above is targeted to the human A₁ adenosine receptor mRNA (EPI 2010). Anti-sense oligo I is 21 nucleotide long, overlaps the initiation codon, and has the following sequence: 5'-GAT GGA GGG CGG CAT GGC GGG-3' (SEQ.ID NO:1). The oligo I was previously shown to abrogate the adenosine-induced bronchoconstriction in allergic rabbits, and to reduce allergen-induced airway obstruction and bronchial hyperresponsiveness (BHR), as discussed above and shown by Nyce, J. W. & Metzger, W. J., Nature, 385:721 (1977), the relevant portions of which reference are incorporated in their entirety herein by reference.

A phosphorothioate anti-sense oligo (SEQ. ID NO:7) was designed in accordance with the invention to target the rabbit adenosine A₁ receptor mRNA region +936 to +956 relative to the initiation codon (start site). The anti-sense oligo II is 21 nucleotide long, and has the following sequence: 5'-CTC GTC GCC GTC GCC GGC GGG-3' (SEQ. ID NO:7).

5 (III) **Anti-sense Oligo III**

A phosphorothioate anti-sense oligo other than that provided in Example 1 above (SEQ. ID NO:8) was designed in accordance with the invention to target the anti-sense A₃ receptor mRNA region +3 to +22 relative to the initiation codon start site. The anti-sense oligo III is 20 nucleotide long, and has the following sequence: 5'-GGG TGG TGC TAT TGT CGG GC-3' (SEQ. ID NO:8).

10 (IV) **Anti-sense Oligo IV**

Yet another phosphorothioate anti-sense oligo (SEQ. ID NO:9) was designed in accordance with the invention to target the adenosine A₃ receptor mRNA region +386 to +401 relative to the initiation codon (start site). The anti-sense oligo IV is 15 nucleotide long, and has the following sequence: 5'-GGC CCA GGC CCA GCC-3' (SEQ. ID NO:9).

15 (V) **Anti-sense Oligo V**

A phosphorothioate anti-sense oligo (SEQ. ID NO:10) was designed in accordance with the invention to target the adenosine A_{2b} receptor mRNA region -21 to -1 relative to the initiation codon (start site). The anti-sense oligonucleotide V is 21 nucleotide long, and has the following sequence: 5'-GGC CGG GCC AGC CGG GCC CGG-3' (SEQ. ID NO:10).

20 (VI) **A₁ Mismatch Oligos**

Two different mismatched oligonucleotides having the following sequences were used as controls for anti-sense oligo I (SEQ. ID NO: 1) described in Example 5 above: A₁ MM2: 5'-GTA GGT GGC GGC CAA GGC GGG-3' (SEQ. ID NO:2421), and A₁ MM3: 5'-GAT GGA GGC GGC CAT GGC GGC-3' (SEQ. ID NO:2422). Anti-sense oligo I and the two mismatch anti-sense oligos had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligo I was specific, not only for the human, but also for the rabbit, adenosine A₁ receptor genes, and that the mismatched controls were not candidates for hybridization with any known human or animal gene sequence.

(VII) **Anti-sense Oligo A₁-PD (Oligo VI)**

30 A phosphodiester anti-sense oligo (Oligo VI; SEQ. ID NO:2420) having the same nucleotide sequence as Oligo I was designed as disclosed in the above-identified application. Anti-sense oligo I-PD is 21 nucleotide long, overlaps the initiation codon, and has the following sequence: 5'-GAT GGA GGC CGG CAT GGC GGC-3' (SEQ. ID NO:2420).

III) Controls

35 Each rabbit was administered 5.0 ml aerosolized sterile saline following the same schedule as for the anti-sense oligos in (II), (III), and (IV) above.

Example 7: Synthesis of Anti-sense Oligos

Phosphorothioate anti-sense oligos having the sequences described in (a) above, were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis. Anti-sense oligonucleotide II (SEQ. ID NO:7), anti-sense oligonucleotide III (SEQ. ID NO: 8) and anti-sense oligonucleotide IV (SEQ. ID NO: 9) were each synthesized and purified in this manner.

Example 8: Preparation of Allergic Rabbits

45 Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp. 347-362, CRC Press, Boca Raton (1990); Ali,

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S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149: 908 (1994)), the relevant portions of which are incorporated in their entirety here by reference. Immunizations were repeated weekly for the first month and then biweekly until the age of 4 months. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (Ali, S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149 (1994)), the relevant section being incorporated in its entirety here by reference.

10 DOSE-RESPONSE STUDIES

Example 9: Experimental Setup

Aerosols of either adenosine (0-20 mg/ml), or anti-sense or one of two mismatch oligonucleotides (5 mg/ml) were separately prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5:μm in diameter. Equal volumes of the aerosols were administered directly to the lungs *via* an intratracheal tube. The animals were randomized, and administered aerosolized adenosine. Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC₅₀ Adenosine). The animals were then administered either the aerosolized anti-sense or one of the mismatch anti-sense oligos *via* the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC₅₀ values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in Example 21 below.

Example 10: Crossover Experiments

For some experiments utilizing anti-sense oligo I (SEQ ID NO: 1) and a corresponding mismatch control oligonucleotide A1MM2, following a 2 week interval, the animals were crossed over, with those previously administered the mismatch control A₁MM2, now receiving the anti-sense oligo I, and those previously treated with the anti-sense oligo I, now receiving the mismatch control A₁MM2 oligo. The number of animals per group was as follows. For mismatch A₁MM2 (Control 1), n=7, since one animal was lost in the second control arm of the experiment due to technical difficulties, for mismatch A₁MM3 n=4 (Control 2) and for A₁AS anti-sense oligo I, n=8. The A₁MM3 oligo-treated animals were analyzed separately and were not part of the cross-over experiment. The treatment methods and measurements employed following the cross-over were identical to those employed in the first arm of the experiment. In 6 of the 8 animals treated with the anti-sense oligo I (SEQ. ID NO: 1), no PC₅₀ value could be obtained for adenosine doses of up to 20 mg/ml, which is the limit of solubility of adenosine. Accordingly, the PC₅₀ values for these animals were assumed to be 20 mg/ml for calculation purposes. The values given, therefore, represent a minimum figure for the effectiveness of the anti-sense oligonucleotides of the invention. Other groups of allergic rabbits (n=4 for each group) were administered 0.5 or 0.05 mg doses of the anti-sense oligo I (SEQ ID NO: 1), or the A₁MM2 oligo in the manner and according to the schedule described above (the total doses being 2.0 or 0.2 mg). The results of these studies are provided in Example 22 below.

40 Example 11: Anti-sense Oligo Formulation

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I (SEQ. ID NO:1) in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer *via* endotracheal tube, as described above. The results obtained for anti-sense oligo I and its mismatch controls confirmed that the mismatch controls are equivalent to saline, as described in Example 19 below and in Table 1 of Nyce & Metzger, Nature 385: 721-725 (1997). Because of this finding, saline was used as a control for pulmonary function studies employing anti-sense oligos II, III and IV (SEQ. IS NOS; 7, 8 and 9).

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Example 12: Specificity of Oligo I for Adenosine A₁ Receptor (Receptor Binding Studies)

Tissue from airway smooth muscle was dissected to primary, secondary and tertiary bronchi from rabbits which had been administered 20 mg oligo I (SEQ ID NO: 1) in 4 divided doses over a period of 48 hours as described above. A membrane fraction was prepared according to the method of Ali et al. (Ali, S., et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994), the relevant section relating to the preparation of the membrane fraction is incorporated in its entirety hereby by reference). The protein content was determined by the method of Bradford and plasma membranes were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37EC to remove endogenous adenosine. See, Bradford, M. M. Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference. The binding of [³H]DPCPX, [³H]NPC17731, or [³H]CGS-21680 was measured as described by Jarvis et al. See, Jarvis, M.F., et al., Pharmacol. Exptl. Ther. 251, 888-893 (1989), the relevant portion of which is fully incorporated herein by reference. The results of this study are shown in Table 8 and discussed in Example 20 below.

Example 13: Pulmonary Function Measurements (Compliance c_{DYN} and Resistance)

At 4 months of age, the immunized animals were anesthetized and relaxed with 1.5 ml of a mixture of ketamine HCl (35 mg/kg) and acepromazine maleate (1.5 mg/kg) administered intramuscularly. After induction of anesthesia, allergic rabbits were comfortably positioned supine on a soft molded animal board. Salve was applied to the eyes to prevent drying, and they were closed. The animals were then intubated with a 4.0 mm intermediate high-low cuffed Murphy 1 endotracheal tube (Mallinckrodt, Glen Falls, NY), as previously described by Zavala and Rhodes. See, Zavala and Rhodes, Proc. Soc. Exp. Biol. Med. 144: 509-512 (1973), the relevant portion of which is incorporated herein by reference in its entirety. A polyethylene catheter of OD 2.4 mm (Becton Dickinson, Clay Adams, Parsippany NJ) with an attached thin-walled latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiment. The endotracheal tube was attached to a heated Fleisch pneumotach (size 00; DEM Medical, Richmond, VA), and the flow (v) measured using a Validyne differential pressure transducer (Model DP-45-16-1927, Validyne Engineering, Northridge, CA), driven by a Gould carrier amplifier (Model 11-4113, Gould Electronics, Cleveland, OH). An esophageal balloon was attached to one side of the Validyne differential pressure transducer, and the other side was attached to the outflow of the endotracheal tube to obtain transpulmonary pressure (P_{tp}). The flow was integrated to yield a continuous tidal volume, and the measurements of total lung resistance (R_L) and dynamic compliance (C_{dyn}) were made at isovolumetric and zero flow points. The flow, volume and pressure were recorded on an eight channel Gould 2000 W high-frequency recorder and C_{dyn} was calculated using the total volume and the difference in P_{tp} at zero flow, and R_L was calculated as the ratio of P_{tp} and V at midtidal lung volumes. These calculations were made automatically with the Buxco automated pulmonary mechanics respiratory analyzer (Model 6, Buxco Electronics, Sharon, CT), as previously described by Giles et al. See, Giles et al., Arch. Int. Pharmacodyn. Ther. 194: 213-232 (1971), the relevant portion of which describing these calculations is incorporated in toto hereby by reference. The results obtained upon administration of oligo II on allergic rabbits are shown and discussed in Example 26 below.

Example 14: Measurement of Bronchial Hyperresponsiveness (BHR)

Each allergic rabbit was administered histamine by aerosol to determine their baseline hyperresponsiveness. Aerosols of either saline or histamine were generated using a DeVilbiss nebulizer (DeVilbiss, Somerset, PA) for 30 seconds and then for 2 minutes at each dose employed. The ultrasonic nebulizer produced aerosol droplets of which 80% were <5 micron in diameter. The histamine aerosol was administered in increasing concentrations (0.156 to 80 mg/ml) and measurements of pulmonary function were made after each dose. The B4R was then determined by calculating the concentration of histamine (mg/ml) required to reduce the C_{dyn} 50% from baseline (PC_{50} Histamine).

Example 15: Cardiovascular Effect of Anti-sense Oligo I

The measurement of cardiac output and other cardiovascular parameters using CardiomaxJ utilizes the principal of thermal dilution in which the change in temperature of the blood exiting the heart after a venous injection of a known volume of cool saline is monitored. A single rapid injection of cool saline was made into the right atrium via cannulation of the right jugular vein, and the corresponding changes in temperature of the mixed injectate and blood in the aortic arch were recorded via cannulation of the carotid artery by a temperature-sensing miniprobe. Twelve hours after the allergic rabbits had been treated with aerosols of oligo I (EPI 2010; SEQ. ID NO: 1) as described in (d) above, the animals were anesthetized with 0.3 ml/kg of 80% Ketamine and 20% Xylazine. This time point coincides with previous data showing efficacy for SEQ. ID NO: 1, as is clearly shown by Nyce & Metzger, (1997), supra, the pertinent disclosure being incorporated in its entirety here by reference. A thermocouple was then inserted into the left carotid artery of each rabbit, and was then advanced 6.5 cm and secured with a silk ligature. The right jugular vein was then cannulated and a length of polyethylene tubing was inserted and secured. A thermodilution curve was then established on a CardiomaxJ II (Columbus Instruments, Ohio) by injecting sterile saline at 20EC to determine the correctness of positioning of the thermocouple probe. After establishing the correctness of the position of the thermocouple, the femoral artery and vein were isolated. The femoral vein was used as a portal for drug injections, and the femoral artery for blood pressure and heart rate measurements. Once constant baseline cardiovascular parameters were established, CardiomaxJ measurements of blood pressure, heart rate, cardiac output, total peripheral resistance, and cardiac contractility were made.

Example 16: Duration of Action of Oligo I (SEQ. ID NO: 1)

Eight allergic rabbits received initially increasing log doses of adenosine by means of a nebulizer via an intra-tracheal tube as described in (f) above, beginning with 0.156 mg/ml until compliance was reduced by 50% (PC_{50} Adenosine) to establish a baseline. Six of the rabbits then received four 5 mg aerosolized doses of (SEQ. ID NO: 1) as described above. Two rabbits received equivalent amounts of saline vehicle as controls. Beginning 18 hours after the last treatment, the PC_{50} Adenosine values were tested again. After this point, the measurements were continued for all animals each day, for up to 10 days. The results of this study are discussed in Example 25 below.

Example 17: Reduction of Adenosine A_{2b} Receptor Number by Anti-sense Oligo V

Sprague Dawley rats were administered 2.0 mg respirable anti-sense oligo V (SEQ ID NO:10) three times over two days using an inhalation chamber as described above. Twelve hours after the last administration, lung parenchymal tissue was dissected and assayed for adenosine A_{2b} receptor binding using [311]-NECA as described by Nyce & Metzger (1997), supra. Controls were conducted by administration of equal volumes of saline. The results are significant at $p < 0.05$ using Student's paired t test, and are discussed in Example 28 below.

Example 18: Comparison of Oligo I & Corresponding Phosphodiester Oligo VI (SEQ. ID NO:1681)

Oligo I (SEQ ID NO:1) countered the effects of adenosine and eliminated sensitivity to it for adenosine amount up to 20 mg adenosine/5.0 ml (the limit of solubility of adenosine). Oligo VI (SEQ ID NO:1681), the phosphodiester version of the oligonucleotide sequence, was completely ineffective when tested in the same manner. Both compounds have identical sequence, differing only in the presence of phosphorothioate residues in Oligo I (SEQ ID NO:1), and were delivered as an aerosol as described above and in Nyce & Metzger (1997), supra. Significantly different at $p < 0.001$, Student's paired t test. The results are discussed in Example 29 below.

Example 19: Results of Prior Work

The nucleotide sequence and other data for anti-sense oligo I (SEQ. ID NO: 1), which is specific for the adenosine A₁ receptor, were provided above. The experimental data showing the effectiveness of oligo I in down regulating the receptor number and activity were also provided above. Further information on the characteristics and activities of anti-sense oligo I is provided in Nyce, J. W. and Metzger, W. J., Nature 385:721 (1997), the relevant parts of which relating to the following results are incorporated in their entireties herein by reference. The Nyce & Metzger (1997) publication provided data showing that the anti-sense oligo I (SEQ. ID NO: 1):

- (1) The anti-sense oligo I reduces the number of adenosine A₁ receptors in the bronchial smooth muscle of allergic rabbits in a dose-dependent manner as may be seen in Table 5 below.
- (2) Anti-sense Oligo I attenuates adenosine-induced bronchoconstriction and allergen-induced bronchoconstriction.
- (3) The Oligo I attenuates bronchial hyperresponsiveness as measured by PC₅₀ histamine, a standard measurement to assess bronchial hyperresponsiveness. This result clearly demonstrates anti-inflammatory activity of the anti-sense oligo I as is shown in Table 5 above.
- (4) As expected, because it was designed to target it, the anti-sense oligo I is totally specific for the adenosine A₁ receptor, and has no effect at all at any dose on either the very closely related adenosine A₂ receptor or the related bradykinin B₂ receptor. This is seen in Table 5 below.
- (5) In contradistinction to the above effects of the Oligo I, the mismatch control molecules MM2 and MM3 (SEQ. ID NO:1682 and SEQ. ID NO:1683) which have identical base composition and molecular weight but differed from the anti-sense oligo I (SEQ ID NO: 1) by 6 and 2 mismatches, respectively. These mismatches, which are the minimum possible while still retaining identical base composition, produced absolutely no effect upon any of the targeted receptors (A₁, A₂ or B₂).

These results, along with a complete lack of prior art on the use of anti-sense oligonucleotides, such as oligo I, targeted to the adenosine A₁ receptor, are unexpected results. The showings presented in this patent clearly enable and demonstrate the effectiveness, for their intended use, of the claimed agents and method for treating a disease or condition associated with lung airway, such as bronchoconstriction, inflammation, allergy(ies), and the like.

Example 20: Oligo I Significantly Reduces Response to Adenosine Challenge

The receptor binding experiment is described in Example 12 above, and the results shown in Table 5 below which shows the binding characteristics of the adenosine A₁-selective ligand [³H]DPCPX and the bradykinin B₂-selective ligand [³H]NPC 17731 in membranes isolated from airway smooth muscle of A₁ adenosine receptor and B₂ bradykinin receptor anti-sense- and mismatch-treated allergic rabbits.

Table 5: Binding Characteristics of Three Anti-Sense Oligos

2 mg	0.39±0.035 nM	44.3±2.90 fmoles	0.34±0.024 nM	11.9±0.76
0.2 mg	0.40±0.028 nM	47.0±3.76 fmoles	0.35±0.028 nM	15.1±1.05 fmoles
B₂MM				
20 mg	0.39±0.031 nM	42.0±2.94 fmoles	0.41±0.029 nM	14.0±0.98 fmoles
2 mg	0.41±0.035 nM	40.0±3.20 fmoles	0.37±0.030 nM	14.8±0.99 fmoles
0.2 mg	0.37±0.029 nM	43.0±3.14 fmoles	0.36±0.025 nM	15.1±1.35 fmoles
Saline Control	0.37±0.041	46.0±5.21	0.39±0.047 nM	14.2±1.35 fmoles

¹ Refers to total oligo administered in four equivalently divided doses over a 48 hour period. Treatments and analyses were performed as described in methods. Significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected t test. n = 4-6 for all groups.

* Significantly different from mismatch control- and saline-treated groups, p<0.001;

**Significantly different from mismatch control- and saline-treated groups, p<0.05.

Example 21: Dose-response Effect of Oligo I

Anti-sense oligo I (SEQ ID NO:1) was found to reduce the effect of adenosine administration to the animal in a dose-dependent manner over the dose range tested as shown in Table 6 below.

Table 6: Dose-Response Effect to Anti-sense Oligo I

Total Dose (mg)	PC ₅₀ Adenosine (mg Adenosine)
Anti-sense Oligo I	
0.2	8.32±7.2
2.0	14.0±7.2
20	19.5±0.34
A₁MM2 oligo (control)	
0.2	2.51±0.46
2.0	3.13± 0.71
20	3.25± 0.34

The above results were studied with the Student's paired t test and found to be statistically different, p=0.05

The oligo I (SEQ. ID NO:1), an anti-adenosine A₁ receptor oligo, acts specifically on the adenosine A₁ receptor, but not on the adenosine A₂ receptors. These results stem from the treatment of rabbits with anti-sense oligo I (SEQ. ID NO:1) or mismatch control oligo (SEQ. ID NO:1682; A₁MM2) as described in Example 9 above and in Nyce & Metzger (1997), supra (four doses of 5 mg spaced 8 to 12 hours apart via nebulizer via endotracheal tube), bronchial smooth muscle tissue excised and the number of adenosine A₁ and adenosine A₂ receptors determined as reported in Nyce & Metzger (1997), supra.

Example 22: Specificity of Oligo I (SEQ. ID NO:1) for Target Gene Product

Oligo I (SEQ. ID No:1) is specific for the adenosine A₁ receptor whereas its mismatch controls had no activity. Figure 1 depicts the results obtained from the cross-over experiment described in Example 10 above and in Nyce & Metzger (1997), supra. The two mismatch controls (SEQ. ID NO:1682 and SEQ. ID NO:1683) evidenced no effect on the PC₅₀ Adenosine value. On the contrary, the administration of anti-sense oligo I (SEQ. ID NO:1) showed a seven-fold increase in the PC₅₀ Adenosine value. The results clearly indicate that the anti-sense oligo I (SEQ. ID NO: 1) reduces the response (attenuates the sensitivity) to exogenously administered adenosine when compared with a saline control. The results provided in Table 6 above clearly establish that the effect of the anti-sense oligo I is dose dependent (see, column 3 of Table 5). The Oligo I was also shown to be totally specific for the adenosine A₁ receptor, (see, top 3 rows of Table), inducing no activity at either the closely related adenosine A₂ receptor or the bradykinin B₂ receptor (see, lines 8-10 of Table 6 above). In addition, the results shown in Table 6 establish that the anti-sense oligo I (SEQ. ID NO:1) decreases sensitivity to adenosine in a dose dependent manner, and that it does this in an

anti-sense oligo-dependent manner since neither of two mismatch control oligonucleotides (A₁MM2; SEQ. ID NO:1682 and A₁MM3; SEQ. ID NO:1683) show any effect on PC₅₀ Adenosine values or on attenuating the number of adenosine A₁ receptors.

**Example 23: Effect on Aeroallergen-induced
Bronchoconstriction & Inflammation**

5 The Oligo I (SEQ. ID NO:1) was shown to significantly reduce the histamine-induced effect in the rabbit model when compared to the mismatch oligos. The effect of the anti-sense Oligo I (SEQ. ID No:1) and the mismatch oligos (A₁MM2, SEQ. ID NO:1682 and A₁MM3, SEQ. ID NO:1682) on allergen-induced airway obstruction and bronchial hyperresponsiveness was assessed in allergic rabbits.

10 The effect of the anti-sense oligo I (SEQ. ID NO:1) on allergen-induced airway obstruction was assessed. As calculated from the area under the plotted curve, the anti-sense oligo I significantly inhibited allergen-induced airway obstruction when compared with the mismatched control (55%, p<0.05; repeated measures ANOVA, and Tukey's t test). A complete lack of effect was induced by the mismatch oligo A₁MM2 (Control) on allergen induced airway obstruction. The effect of the anti-sense oligo I (SEQ. ID NO:1) on

15 allergen-induced BHR was determined as above. As calculated from the PC₅₀ Histamine value, the anti-sense oligo I (SEQ. ID NO:1) significantly inhibited allergen-induced BHR in allergic rabbits when compared to the mismatched control (61%, p<0.05; repeated measures ANOVA, Tukey's t test). A complete lack of effect of the A₁MM mismatch control on allergen-induced BHR was observed. The results indicated that anti-sense oligo I (SEQ. ID NO: 1) is effective to protect against aeroallergen-induced bronchoconstriction

20 (house dust mite). In addition, the anti-sense oligo I (SEQ. ID NO:1) was also found to be a potent inhibitor of dust mite-induced bronchial hyper responsiveness, as shown by its effects upon histamine sensitivity which indicates anti-inflammatory activity for anti-sense oligo I (SEQ. ID NO:1).

Example 24: Anti-sense Oligo I is Free

NO:1) had disappeared, the animals were administered saline aerosols (controls), and the PC₅₀ Adenosine values for all animals were measured again. Saline-treated animals showed base line PC₅₀ adenosine values (n=6). The duration of the effect (with respect to Resistance) was measured for six allergic rabbits which were administered 20 mg of anti-sense oligo I (SEQ. ID NO: 1) as described above, upon airway resistance measured as also described above. The mean calculated duration of effect was 8.3 days for both PC₅₀ adenosine (p<0.05) and resistance (p<0.05). These results show that anti-sense oligo I (SEQ. ID NO:1) has an extremely long duration of action, which is completely unexpected.

Example 26: Anti-sense Oligo II

Anti-sense oligo II, targeted to a different region of the adenosine A₁ receptor mRNA, was found to be highly active against the adenosine A₁-mediated effects. The experiment measured the effect of the administration of anti-sense oligo II (SEQ. ID NO:7) upon compliance and resistance values when 20 mg anti-sense oligo II or saline (control) were administered to two groups of allergic rabbits as described above. Compliance and resistance values were measured following an administration of adenosine or saline as described above in Example 13. The effect of the anti-sense oligo of the invention was different from the control in a statistically significant manner, p<0.05 using paired t-test, compliance; p<0.01 for resistance. The results showed that anti-sense oligo II (SEQ. ID NO:7), which targets the adenosine A₁ receptor, effectively maintains compliance and reduces resistance upon adenosine challenge.

Example 27: Antisense Oligos III and IV

Oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) were shown to be in fact specifically targeted to the adenosine A₃ receptor by their effect on reducing inflammation and the number of inflammatory cells present upon separate administration of 20 mg of the anti-sense oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) to allergic rabbits as described above. The number of inflammatory cells was determined in their bronchial lavage fluid 3 hours later by counting at least 100 viable cells per lavage. The effect of anti-sense oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) upon granulocytes, and upon total cells in bronchial lavage were assessed following exposure to dust mite allergen. The results showed that the anti-sense oligo IV (SEQ. ID NO:9) and anti-sense oligo III (SEQ. ID NO:8) are very potent anti-inflammatory agents in the asthmatic lung following exposure to dust mite allergen. As is known in the art, granulocytes, especially eosinophils, are the primary inflammatory cells of asthma, and the administration of anti-sense oligos III (SEQ. ID NO:8) and IV (SEQ. ID NO:9) reduced their numbers by 40% and 66%, respectively. Furthermore, anti-sense oligos IV (SEQ. ID NO:9) and III (SEQ. ID NO:8) also reduced the total number of cells in the bronchial lavage fluid by 40% and 80%, respectively. This is also an important indicator of anti-inflammatory activity by the present anti-adenosine A₃ agents of the invention. Inflammation is known to underlie bronchial hyperresponsiveness and allergen-induced bronchoconstriction in asthma. Both anti-sense oligonucleotides III (SEQ. ID NO:8) and IV (SEQ. ID NO:9), which are targeted to the adenosine A₃ receptor, are representative of an important new class of anti-inflammatory agents which may be designed to specifically target the lung receptors of each species.

Example 28: Anti-sense Oligo V

The anti-sense oligo V (SEQ. ID NO:10), targeted to the adenosine A_{2b} adenosine receptor mRNA was shown to be highly effective at countering adenosine A_{2b}-mediated effects and at reducing the number of adenosine A_{2b} receptors present to less than half.

Example 29: Unexpected Superiority of Substituted over Phosphodiester-residue Oligo I-DS (SEQ. ID NO:1681)

Oligos I (SEQ. ID NO:1) and I-DS (SEQ. ID NO:1681) were separately administered to allergic rabbits as described above, and the rabbits were then challenged with adenosine. The phosphodiester oligo I-DS (SEQ. ID NO:1681) was statistically significantly less effective in countering the effect of adenosine

Example 30: Anti-sense Oligo VI

For the present work, I designed an additional anti-sense phosphorothioate oligo targeted to the adenosine A₁ receptor (Oligo VI). This anti-sense oligo was designed for therapy on a selected species as described in the above patent application and is generally specific for that species, unless the segment of the adenosine receptor mRNA of other species elected happens to have a similar sequence. The anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and lung allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application. One additional oligo and its effect in a rabbit model was studied and the results of the study are reported and discussed below. The present oligo (anti-sense oligo VI) was selected for this study to complement the data on SEQ ID NO: 1 (Oligo I), which is anti-sense to the adenosine A₁ receptor mRNA provided in the above-identified patent application. This additional oligo is identified as anti-sense Oligo VI, and is targeted to a different region of the adenosine A₁ receptor mRNA than Oligo I. The design and synthesis of this anti-sense oligo was performed in accordance with the teaching, particularly Example 1, of the above-identified patent application. The anti-sense Oligo VI is a phosphorothioate designed to target the coding region of the rabbit adenosine A₁ receptor mRNA region +964 to +984 relative to the initiation codon (start site). The Oligo VI was prepared as described in the above-indicated application, and is 20 nucleotides long. The Oligo VI is directed to the adenosine A₁ receptor gene, and has the following sequence: 5'-CGC CGG CGG GTG CGG GCC GG-3' (SEQ. ID NO: 1). The phosphorothioate anti-sense Oligo VI having the sequence described in (5) above, was synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis.

Example 31: Preparation of Allergic Rabbits

Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp 347-362, CRC Press, Boca Raton, 1990; Ali, S. Et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994)). The immunizations were repeated weekly for the first month and then bi-weekly until the animals were 4 months old. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (1994), supra.

Example 32: Adenosine Aerosol Preparation

An adenosine aerosol (20 mg/ml) was prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5:μm in diameter. Equal volumes of the aerosols were administered directly to the lungs via an intratracheal tube to all three rabbits. The animals were then administered the aerosolized adenosine and Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC₅₀ Adenosine). The animals were then administered the aerosolized anti-sense via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC₅₀ values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in (9) below.

Example 33: Anti-sense Oligo Formulation

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above.

Example 34: Oligo VI Reduces Response to Adenosine Challenge as well or Better than Oligo I

Oligo VI was tested in three allergic rabbits of the characteristics and readied as described in (7) above and in the above-indicated patent application. Oligo VI targets a section of the coding region of the A₁ receptor which is different from Oligo I. Both these target sequences were selected randomly from many possible coding region target sequences. The three rabbits were treated identically as previously indicated for Oligo I. Briefly, 5 mg of Oligo VI were nebulized to the rabbits twice per day at 8 hour intervals, for two days. Thereafter, PC₅₀ adenosine studies were performed on the morning of the third day and compared to pre-treatment PC₅₀ values. This protocol is described in more detail in Nyce and Metzger (Nyce & Metzger, Nature 385: 721-725 (1997)). The results obtained for the three rabbits are shown in Table 7 below.

Table 7: PC₅₀ Adenosine before & after Aerosolized Adenosine Treatment

Treatment Time	PC ₅₀ Adenosine (mg)
Pre-treatment	3.0 ± 2.1
Post-treatment	>20.0*

* maximum achievable dose due to adenosine insolubility in saline

All three animals treated with Oligo VI completely eliminated sensitivity to adenosine up to the measurable level of the agent shown in Table 7 above. That is, the administration of the Oligo VI abrogated the adenosine-induced bronchoconstriction in the three allergic rabbits. The actual efficacy of Oligo VI is, therefore, greater than could be measured in the experimental system used. By comparing with the previously submitted results for the Oligo I, it may be seen that the Oligo VI was found to be as effective, or more, than Oligo I.

Example 34: Conclusions

The work described and results discussed in the examples clearly indicates that all anti-sense oligonucleotides designed in accordance with the teachings of the above-identified application were found to be highly effective at countering or reducing effects mediated by the receptors they are targeted to. That is, each and all of the two anti-sense oligos targeting an adenosine A₁ receptor mRNA, 1 anti-sense oligo targeting an adenosine A_{2b} receptor mRNA, and the 2 anti-sense oligos targeting an A₃ receptor mRNA were shown capable of countering the effect of exogenously administered adenosine which is mediated by the specific receptor they are targeted to. The activity of the anti-sense oligos of this invention, moreover, is specific to the target and substitutively fails to inhibit another target. In addition, the results presented also show that the administration of the present agents results in extremely low or non-existent deleterious side effects or toxicity. This represents 100% success in providing agents that are highly effective and specific in the treatment of bronchoconstriction and/or inflammation. This invention is broadly applicable in the same manner to all gene(s) and corresponding mRNAs encoding proteins involved in or associated with airway diseases. A comparison of the phosphodiester and a version of the same oligonucleotide wherein the phosphodiester bonds are substituted with phosphorothioate bonds evidenced an unexpected superiority for the phosphothiorate oligonucleotide over the phosphodiester anti-sense oligo.

Example 35: In Vivo Response to Adenosine Challenge with & without Oligo I Pretreatment

Two hyper responsive monkeys (ascaris sensitive) were challenged with inhaled adenosine, with and without pre-treatment with anti-sense oligo I (SEQ.ID NO: 1). The PC₄₀ adenosine was calculated from the data collected as being equivalent to that amount of adenosine in mg that causes a 40% decrease in dynamic compliance in hyper-responsive airways. The Oligo I (SEQ. ID NO:1; EPI 2010) was subsequently administered at 10 mg/day for 2 days by inhalation. On the third day, the PC adenosine was again measured. The PC₄₀ adenosine value prior to treatment with Oligo I was compared side-by-side with

to the PC₄₀ adenosine taken after administration of Oligo I (Figure not shown). The results of the experiment conducted with two animals showed that any sensitivity to adenosine was completely eliminated by the administration of the oligo of this invention in one animal, and substantially reduced in the second.

5 **Example 36: Extension of the experimental Results**

- The method of the present invention is also practiced with anti-sense oligonucleotides targeted to many genes, mRNAs and their corresponding proteins as described above, in essentially the same manner as given above, for the treatment of various conditions in the lungs. Examples of these are Human A2a adenosine receptor, Human A2b adenosine receptor, Human IgE receptor β , Human Fc-epsilon receptor
- 10 CD23 antigen (IgE receptor), Human IgE receptor, α subunit, Human IgE receptor, Fc epsilon R, Human histidine decarboxylase, Human beta tryptase, Human tryptase-I, Human prostaglandin D synthase, Human cyclooxygenase-2, Human eosinophil cationic protein, Human eosinophil derived neurotoxin, Human eosinophil peroxidase, Human intercellular adhesion molecule-1 (CAM-1), Human vascular cell adhesion molecule 1 (VCAM-1), Human endothelial leukocyte adhesion molecule (ELAM-1), Human P Selectin,
- 15 Human endothelial monocyte activating factor, Human IL3, Human IL4, Human IL5, Human IL6, Human monocyte-derived neutrophil chemotactic factor, Human neutrophil elastase (medullasin), Human neutrophil oxidase factor, Human cathepsin G, Human defensin 1, Human defensin 3, Human macrophage inflammatory protein-1-alpha, Human muscarinic acetylcholine receptor HM1, Human muscarinic acetylcholine receptor HM3, Human fibronectin, Human interleukin 8, Human GM-CSF, Human tumor
- 20 necrosis factor α , Human leukotriene C4 synthase, Human major basic protein, and many more.

The foregoing examples are illustrative of the present invention, and are not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

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